

98	36	58.1	462	2	AAV34339	AAV34339	Porthocym
99	36	58.1	462	2	AAU40023	AAU40023	Protein e
100	36	58.1	468	6	AAU41641	AAU41641	Protein e
101	36	58.1	533	6	AAU27821	AAU27821	Protein e
102	36	58.1	632	8	AAU95021	AAU95021	Plant ful
103	36	58.1	632	8	AAU95021	AAU95021	Plant ful
104	36	58.1	883	1	AAU62141	AAU62141	Drosophi
105	36	58.1	976	6	AAU03087	AAU03087	Alpha aci
106	36	58.1	976	6	AAU07388	AAU07388	Alpha aci
107	36	58.1	1016	1	AAU94035	AAU94035	Delta-end
108	36	58.1	1180	1	AAU94035	AAU94035	Delta-end
109	36	58.1	1180	1	AAU93715	AAU93715	Insectic
110	36	58.1	1180	2	AAU14373	AAU14373	Dipteran
111	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
112	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
113	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
114	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
115	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
116	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
117	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
118	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
119	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
120	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
121	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
122	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
123	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
124	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
125	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
126	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
127	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
128	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
129	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
130	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
131	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
132	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
133	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
134	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
135	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
136	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
137	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
138	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
139	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
140	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
141	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
142	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
143	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
144	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
145	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
146	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
147	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
148	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
149	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
150	36	58.1	1180	2	AAU63078	AAU63078	B. t. coxi
151	36	58.1	1180	2	AAU63078	AAU6	

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:12 ; Search time 12.8571 Seconds
(without alignments)
104.769 Million cell updates/sec

Title: US-10-067-484-1
Perfect score: 62
Sequence: 1 XXSGISNTVYANPK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	66.1	382	2	E83846 D-alanyl-D-alanine
2	39	62.9	673	2	T47905 hypothetical prote
3	39	62.9	1024	2	C64208 hypothetical prote
4	38	61.3	336	2	F82242 oligopeptide ABC t
5	37	59.7	93	2	D69262 hypothetical prote
6	37	59.7	339	2	E84671 hypothetical prote
7	37	59.7	389	2	H81146 penicillin-binding
8	37	59.7	389	2	D81875 probable serine-ty
9	37	59.7	562	2	S44287 pyruvate kinase, p
10	37	59.7	653	2	F70383 organic solvent to
11	37	59.7	830	2	E83031 conserved hypothet
12	37	59.7	1751	2	G71518 hypothetical prote
13	36	58.1	117	2	C64378 hypothetical prote
14	36	58.1	205	2	AC3366 serine-type D-Ala-
15	36	58.1	243	2	S43887 restriction endonu
16	36	58.1	243	2	F81130 type II restrictio
17	36	58.1	507	2	E64247 phosphoglycerate m
18	36	58.1	969	2	T15446 hypothetical prote
19	36	58.1	1180	2	A26858 paraformal crystal
20	36	58.1	1180	2	I39870 parafornal crystal
21	35.5	57.3	981	2	C96712 hypothetical prote
22	35	56.5	225	2	A97735 hypothetical prote
23	35	56.5	310	2	AB0275 arabinose operon r
24	35	56.5	343	2	AG1273 N-acetylglutamate
25	35	56.5	343	2	AH1636 N-acetylglutamate
26	35	56.5	442	2	T14353 probable 4-hydroxy
27	35	56.5	456	2	E86903 hypothetical prote
28	35	56.5	469	2	AC2794 glutamine syntheta
29	35	56.5	469	2	B97573 glutamine syntheta

30	35	56.5	469	2	AB3374 glutamate-ammonia
31	35	56.5	473	2	S75141 glutamate-synthase
32	35	56.5	522	2	S55982 asparagine synthase
33	35	56.5	591	2	A99444 acylaminoacyl-pept
34	35	56.5	657	2	T24605 hypothetical prote
35	35	56.5	716	2	AB6181 hypothetical prote
36	35	56.5	939	2	AE2275 hypothetical prote
37	35	56.5	1545	2	B41859 Iga-specific metal
38	35	56.5	1802	2	G71616 hypothetical prote
39	34.5	55.6	2076	2	S15999 fatty-acyl-CoA sym
40	34	54.8	72	2	G97134 hypothetical prote
41	34	54.8	75	2	AB6487 unknown protein li
42	34	54.8	131	2	G72653 hypothetical prote
43	34	54.8	169	2	E97775 hypothetical prote
44	34	54.8	227	2	T06362 probable 2-oxoglut
45	34	54.8	263	2	AB2069 hypothetical prote
46	34	54.8	342	2	S57814 oxidase like prote
47	34	54.8	342	2	H84898 hypothetical prote
48	34	54.8	389	2	AH3003 penicillin-binding
49	34	54.8	398	2	A99280 conserved hypothet
50	34	54.8	408	2	S66705 conserved hypothet
51	34	54.8	423	2	A90450 ATP-dependent RNA
52	34	54.8	443	2	AB2872 dipeptidase (impor
53	34	54.8	474	2	F86819 glutamate-ammonia
54	34	54.8	476	2	F81340 hypothetical prote
55	34	54.8	479	2	T02623 hypothetical prote
56	34	54.8	481	2	G86144 hypothetical prote
57	34	54.8	485	2	S17050 H+-exporting ATPas
58	34	54.8	495	2	B85964 hypothetical prote
59	34	54.8	495	2	C91119 outer membrane cha
60	34	54.8	512	2	T41340 hypothetical prote
61	34	54.8	518	2	E87754 protein C43E1.10
62	34	54.8	532	1	CPBYV carboxypeptidase C
63	34	54.8	550	2	B97346 oligopeptide ABC t
64	34	54.8	570	2	B97160 fibronectin-bindin
65	34	54.8	594	2	D64676 oligopeptide ABC t
66	34	54.8	595	2	D71841 hypothetical prote
67	34	54.8	605	1	A35459 glucose oxidase (B
68	34	54.8	645	2	F70825 probable PPE prote
69	34	54.8	704	2	S76120 hypothetical prote
70	34	54.8	766	2	C87689 NAD-dependent mal
71	34	54.8	781	2	B56939 isoquinoline 1-oxi
72	34	54.8	875	2	T50182 ubiquitin-specific
73	34	54.8	961	2	S67568 G protein-coupled
74	34	54.8	962	2	JC5808 hypothetical prote
75	34	54.8	1286	1	S38058 unknown protein ri
76	34	54.8	2599	2	A96616 glutamate synthase
77	34	54.8	3097	2	T28635 probable PPE prote
78	34	54.8	3300	2	D70575 hypothetical 367K
79	34	54.8	3472	2	T31308 phenazine biosynth
80	33.5	54.0	290	2	AF3234 jacalin beta-1 cha
81	33	53.2	20	2	S29636 hypothetical prote
82	33	53.2	77	2	T20897 hypothetical prote
83	33	53.2	116	1	BVECBA bola protein - Bsc
84	33	53.2	116	2	A90690 probable regulator
85	33	53.2	116	2	B85540 probable murein ge
86	33	53.2	155	2	A28083 glutathione transf
87	33	53.2	162	2	B90402 hypothetical prote
88	33	53.2	181	2	S75415 probable ribosomal
89	33	53.2	196	1	G8P884 basophilic protein
90	33	53.2	217	2	A46630 jacalin precursor
91	33	53.2	228	1	OXASC NADH2 dehydrogenas
92	33	53.2	291	2	S15927 sfah protein precu
93	33	53.2	297	2	H70446 UTP-glucose-1-phos
94	33	53.2	299	2	C49233 S fibribrial adhesin
95	33	53.2	299	2	I76900 F162 minor fibridi
96	33	53.2	302	2	D81393 probable lyase Cj0
97	33	53.2	302	2	T45937 hypothetical prote
98	33	53.2	306	2	AC0602 probable exported
99	33	53.2	306	2	H90740 hypothetical prote
100	33	53.2	306	2	C64819 ybIs protein precu
101	33	53.2	306	2	C85591 hypothetical prote
102	33	53.2	309	2	AB0757 probable exported

103	33	53.2	310	2	A99977	176	32	51.6	105	2	A10557	Bola protein (limp
104	33	53.2	310	2	G83823	177	32	51.6	109	2	C84974	protein-export mem
105	33	53.2	310	2	G83823	178	32	51.6	116	2	AB2360	hypothetical prote
106	33	53.2	320	2	H8548	179	32	51.6	145	2	T22693	hypothetical prote
107	33	53.2	320	2	H84816	180	32	51.6	170	2	AF3369	xanthine phosphori
108	33	53.2	320	2	B84150	181	32	51.6	186	2	TS0361	hypothetical prote
109	33	53.2	332	2	F75473	182	32	51.6	207	2	C83875	hypothetical prote
110	33	53.2	332	2	F75473	183	32	51.6	211	2	AF0175	conserved hypothet
111	33	53.2	336	2	H72428	184	32	51.6	223	2	JC5903	coat protein - Cym
112	33	53.2	336	2	C86821	185	32	51.6	231	2	C70439	DNA repair protein
113	33	53.2	389	2	B82479	186	32	51.6	232	2	G70738	probable PPE prote
114	33	53.2	389	2	AG2018	187	32	51.6	251	2	B82027	probable MAFs alte
115	33	53.2	395	2	E84009	188	32	51.6	275	2	JC6181	phosphate ABC tran
116	33	53.2	397	2	D89768	189	32	51.6	281	2	T38802	RNA polymerase II
117	33	53.2	425	2	S74939	190	32	51.6	281	2	T38802	hypothetical prote
118	33	53.2	425	2	H70410	191	32	51.6	307	2	E90402	hypothetical prote
119	33	53.2	442	2	E70069	192	32	51.6	319	2	AI0307	flagellin, probabl
120	33	53.2	442	2	A45709	193	32	51.6	322	2	AI0307	probable glycosyl
121	33	53.2	451	2	T41877	194	32	51.6	322	2	B64382	formylmethanofuran
122	33	53.2	451	2	T41911	195	32	51.6	325	2	C69805	iron(III) dicitrat
123	33	53.2	453	2	T24127	196	32	51.6	327	2	F90180	sun (fmu) protein
124	33	53.2	463	2	S16530	197	32	51.6	339	2	G75529	peptide ABC transp
125	33	53.2	469	2	D81784	198	32	51.6	341	2	B70663	hypothetical prote
126	33	53.2	472	2	B81784	199	32	51.6	354	2	B70663	probable PPE prote
127	33	53.2	473	2	H85482	200	32	51.6	358	2	H83167	bioB/LiPA-like pro
128	33	53.2	473	2	H85482	201	32	51.6	367	2	H93115	probable transfe
129	33	53.2	473	2	A90632	202	32	51.6	370	2	I40085	gcs protein - Bac
130	33	53.2	485	2	C86336	203	32	51.6	386	2	F95911	probable mutase
131	33	53.2	487	2	T05679	204	32	51.6	386	2	B85906	chorismate hydrocarb
132	33	53.2	488	2	T43789	205	32	51.6	389	2	F91061	chorismate mutase-
133	33	53.2	492	2	A31886	206	32	51.6	389	2	B42708	serine-type D-Ala-
134	33	53.2	495	2	A48370	207	32	51.6	389	2	B42708	surface antigen -
135	33	53.2	496	2	T50146	208	32	51.6	389	2	S20753	hypothetical prote
136	33	53.2	499	2	C71895	209	32	51.6	391	2	C71302	conserved hypotet
137	33	53.2	520	2	D64618	210	32	51.6	397	2	S42039	oxalate/formate an
138	33	53.2	526	2	G96788	211	32	51.6	408	2	G83406	probable symporter
139	33	53.2	526	2	T23779	212	32	51.6	418	2	T47239	transcription fact
140	33	53.2	545	2	D90159	213	32	51.6	422	2	AF0072	zinc finger protei
141	33	53.2	575	1	WOEBPI	214	32	51.6	433	2	A56953	probable membrane
142	33	53.2	575	1	WOEBPI	215	32	51.6	446	2	T01524	protein F57B9.10
143	33	53.2	575	2	C85884	216	32	51.6	467	2	AG1059	glutamine syntheta
144	33	53.2	575	2	H91039	217	32	51.6	469	2	H88493	glutamate-amonita
145	33	53.2	585	2	HE4137	218	32	51.6	472	2	G83005	polysaccharide bio
146	33	53.2	584	2	E71687	219	32	51.6	475	2	F81208	glutamate-amonita
147	33	53.2	610	2	E97753	220	32	51.6	479	2	D86651	polysaccharide bio
148	33	53.2	610	2	T39485	221	32	51.6	479	2	F82432	cell cycle control
149	33	53.2	658	2	T05655	222	32	51.6	481	2	T46606	hypothetical prote
150	33	53.2	664	2	T48258	223	32	51.6	481	2	T46606	hypothetical prote
151	33	53.2	738	2	T44194	224	32	51.6	497	2	T19077	alpha-amylase (Bc
152	33	53.2	738	2	T44007	225	32	51.6	528	1	ALBSK	hypothetical prote
153	33	53.2	754	2	JC4898	226	32	51.6	534	2	S31300	regulatory protein
154	33	53.2	782	2	AE2262	227	32	51.6	534	2	S31300	hypothetical prote
155	33	53.2	783	2	AE2262	228	32	51.6	538	2	S76085	hypothetical prote
156	33	53.2	895	2	A45554	229	32	51.6	540	2	B40901	equine arteritis v
157	33	53.2	943	2	B45082	230	32	51.6	547	2	C84593	probable sugar tra
158	33	53.2	1073	2	T01955	231	32	51.6	554	2	B82934	hypothetical prote
159	33	53.2	1178	2	S76370	232	32	51.6	558	2	E70756	hypothetical glyci
160	33	53.2	1212	2	C82834	233	32	51.6	560	2	A86214	hypothetical prote
161	33	53.2	1230	2	T07663	234	32	51.6	574	2	G83794	hypothetical prote
162	33	53.2	1265	2	F84517	235	32	51.6	575	2	AC0364	phosphonolpyruvat
163	33	53.2	1310	2	AD1380	236	32	51.6	599	2	S15004	hypothetical prote
164	33	53.2	1367	2	A11228	237	32	51.6	610	2	G86407	hypothetical prote
165	33	53.2	1369	2	T15654	238	32	51.6	613	2	T19677	hypothetical prote
166	33	53.2	1571	2	S50669	239	32	51.6	619	2	B82141	peptidyl-prolyl ci
167	33	53.2	1678	2	D86481	240	32	51.6	633	1	A26030	serine/chreonine-s
168	33	53.2	1732	2	T08036	241	32	51.6	637	2	YCRP	acetoacetate synth
169	33	53.2	2032	2	T39917	242	32	51.6	638	2	S22490	acetoacetate synth
170	33	53.2	2049	2	T47587	243	32	51.6	638	2	S22491	acetoacetate synth
171	33	53.2	2408	2	T24463	244	32	51.6	652	2	S29838	acetoacetate synth
172	33	53.2	2628	2	T8651	245	32	51.6	655	2	S17691	acyl-CoA dehydroge
173	33	52.4	182	2	G43901	246	32	51.6	655	2	AS4872	acetyl-CoA dehydroge
174	32.5	52.4	163	2	T30290	247	32	51.6	659	2	S60056	acetyl-CoA dehydroge
175	32	51.6	87	2	A55846	248	32	51.6	659	2	S60056	acetyl-CoA dehydroge

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:05 ; Search time 76.2857 Seconds
(without alignments)
129.479 Million cell updates/sec

Title: US-10-067-484-1
Perfect score: 62
Sequence: 1 XXSGISNTVYANPK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database: UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	69.4	666	2	05VGY1_PLAFA
2	43	69.4	666	2	08IAZ6_PLAFA
3	43	69.4	1564	2	08ISW4_PLAFA
4	42	67.7	242	2	05SPD1_CRYNE
5	42	67.7	242	2	05KE25_CRYNE
6	42	67.7	540	2	04MP87_BACCE
7	42	67.7	540	2	06HHP3_BACCH
8	42	67.7	540	2	08ICCS_BACCR
9	42	67.7	540	2	08IPF9_BACAN
10	42	67.7	540	2	063AA2_BACAZ
11	42	67.7	899	2	04N9L5_THBPA
12	42	67.7	1242	2	04XZJ9_PLACH
13	41	66.1	75	2	05BQZ4_SCHUA
14	41	66.1	106	2	04VC39_HUMAN
15	41	66.1	382	2	09KCB8_BACHD
16	41	66.1	1972	2	06MS19_MYCMS
17	40	64.5	355	2	07UP11_RHOBA
18	40	64.5	620	2	08MSK2_TRYBB
19	40	64.5	769	2	04P7V3_USUMA
20	40	64.5	1098	2	05OPJ3_ENTHI
21	39	62.9	106	2	09BW72_HUMAN
22	39	62.9	106	2	09CQJ1_MOUSE
23	39	62.9	229	2	04YV99_PLABH
24	39	62.9	229	2	04Y037_PLACH
25	39	62.9	258	2	04FMB9_GRICK
26	39	62.9	250	2	08RGL2_FUSNN
27	39	62.9	276	2	07RKK7_PLAFA
28	39	62.9	278	2	08IDP1_PLAFA
29	39	62.9	342	2	07RK05_PLAFA
30	39	62.9	505	1	GCSPB_SUITO
31	39	62.9	584	2	08RGS8_FUSNN

32	39	62.9	639	2	094B28_ARATH	094b28 arabidopsis
33	39	62.9	655	2	0869S4_DICDI	0869s4 dictyostell
34	39	62.9	673	2	09LES9_ARATH	09les9 arabidopsis
35	39	62.9	698	2	0554Z5_DICDI	0554z5 dictyostell
36	39	62.9	786	2	05NRA2_ZYMO	05nra2 zymomonas m
37	39	62.9	905	2	04UG55_THBAN	04ug55 theileria a
38	39	62.9	1024	1	Y075_MYCB	P47321 mycoplasma
39	39	62.9	1476	2	08TFN3_NEUCR	08tfn3 neurospora
40	39	62.9	1520	2	07S8U6_NEUCR	07s8u6 neurospora
41	38	61.3	67	2	07P3N2_FUSNN	07p3n2 fusobacteri
42	38	61.3	99	2	05VOC7_HALMA	05voc7 haloarcula
43	38	61.3	125	2	04WVX3_BACCE	04wvx3 bacillus ce
44	38	61.3	204	2	07IAE7_9NOCL	07iae7 manestira co
45	38	61.3	204	2	08QIG9_NPYMC	08qig9 manestira co
46	38	61.3	258	2	05GRV9_WOLTR	05grv9 wolbachia s
47	38	61.3	314	2	0658X8_HUMAN	0658x8 homo sapien
48	38	61.3	314	2	068F68_XENTA	068f68 xenopus lae
49	38	61.3	315	2	06CAL3_YARLI	06cal3 yarrowia li
50	38	61.3	323	2	09H635_HUMAN	09h635 homo sapien
51	38	61.3	333	2	09P5R5_VIBCH	09p5r5 vibrio chol
52	38	61.3	336	2	09KTI0_VIBCH	09kti0 vibrio chol
53	38	61.3	356	1	ASCC1_MOUSE	09ad821 mus musculu
54	38	61.3	356	2	05XIII_RAT	05xiii rattus norv
55	38	61.3	380	2	05WGG2_BACSK	05wgg2 bacillus cl
56	38	61.3	400	2	06CFI7_YARLI	06cfi7 yarrowia li
57	38	61.3	432	2	0874D8_ORPSP	0874d8 orpinomyces
58	38	61.3	432	2	0874E0_ORPSP	0874e0 orpinomyces
59	38	61.3	459	2	055FP6_DICDI	055fp6 dictyostell
60	38	61.3	512	2	05RCY4_PONPY	05rcy4 pongo pygma
61	38	61.3	522	2	08R585_MOUSE	08r585 mus musculu
62	38	61.3	635	2	04R6K0_MACFA	04r6k0 macaca faec
63	38	61.3	690	2	08BP56_MOUSE	08bp56 m mus muscu
64	38	61.3	910	2	0591W8_CANAL	0591w8 candida alb
65	38	61.3	1001	2	05A3N0_CANAL	05a3n0 candida alb
66	38	61.3	1012	2	05A3U5_CANAL	05a3u5 candida alb
67	38	61.3	1031	2	05B612_EMENI	05b612 aspergillus
68	38	61.3	1137	2	055CG8_DICDI	055cg8 dictyostell
69	38	61.3	1542	2	07SFA8_NEUCR	07sfa8 neurospora
70	37	59.7	93	1	Y100_ARCFU	030136 archaeoglob
71	37	59.7	127	2	05ICJ4_BACFN	05icj4 bacteroides
72	37	59.7	127	2	06ATP3_BACFR	06atp3 bacteroides
73	37	59.7	127	2	08UM88_9NOCL	08um88 manestira co
74	37	59.7	223	2	06UTY3_9VIRU	06uty3 cybindidum m
75	37	59.7	223	2	06UTY4_9VIRU	06uty4 cybindidum m
76	37	59.7	234	2	05XVD4_ARATH	05xvd4 arabidopsis
77	37	59.7	257	2	073IK7_WOLPM	073ik7 wolbachia p
78	37	59.7	268	2	04I172_AZOVI	04i172 azotobacter
79	37	59.7	297	2	07RGDS_PLAFA	07rgds plasmodium
80	37	59.7	319	2	06BQZ9_DEBHA	06bz29 debaryomyce
81	37	59.7	321	2	07RSQ0_PLAFA	07rsq0 plasmodium
82	37	59.7	323	2	05BPS8_ARATH	05bps8 arabidopsis
83	37	59.7	323	2	05YVD5_ARATH	05yvd5 arabidopsis
84	37	59.7	336	2	05FP05_GUOX	05fp05 gluconobact
85	37	59.7	339	2	09XIN9_ARATH	09xin9 arabidopsis
86	37	59.7	369	2	09P808_9FUNG	09p8q8 piromyces t
87	37	59.7	389	2	05FP93_NEIG1	05fp93 neisseria g
88	37	59.7	389	2	09JUX6_NEIMA	09jux6 neisseria m
89	37	59.7	389	2	09JXW2_NEIMA	09jxw2 neisseria m
90	37	59.7	409	2	07BR32_STRCL	07br32 streptomyce
91	37	59.7	412	2	06EH22_NEORF	06eh22 neocallimas
92	37	59.7	414	2	09VBS3_DROME	09vbs3 drosophila
93	37	59.7	428	2	012646_NEOPA	012646 neocallimas
94	37	59.7	429	2	06EY63_9FUNG	06ey63 neocallimas
95	37	59.7	474	2	08KZZ2_CHLTR	08kzz2 chlorobium
96	37	59.7	484	2	07VE91_HELHP	07ve91 helicobacte
97	37	59.7	498	2	057ZFS_9TRIP	057zfs trypanosoma
98	37	59.7	510	2	06ELIY8_NEOFR	06eliy8 neocallimas
99	37	59.7	550	2	04KKU3_HUMAN	04kku3 homo sapien
100	37	59.7	562	1	KPYG_TOBAC	040546 nicotiana t
101	37	59.7	574	2	051WS7_TORAC	051ws7 nicotiana t
102	37	59.7	586	2	06PPZ1_CANGA	06ppz1 candida gla
103	37	59.7	586	2	04WDB8_ASFPU	04wdb8 aspergillus
104	37	59.7	589	2	07WBQ2_BORPA	07wbq2 bordetella

105	37	59.7	599	2	Q7MM6 BORBR	Q7mmb6 bordetella	178	36	58.1	598	2	Q4XM84 PLACH	Q4xm84 plasmodium
106	37	59.7	591	2	Q9M3Y6 CICAR	Q9m3y6 cicer ariet	179	36	58.1	607	2	Q7XK60 NEUCR	Q7xk60 neurospora
107	37	59.7	653	2	Q67097 AQUAR	Q67097 aquile arde	180	36	58.1	607	2	Q17795 NEUCR	Q17795 neurospora
108	37	59.7	696	2	Q54201 STRCL	Q54201 streptococ	181	36	58.1	611	2	Q8N155 NEUCR	Q8n155 neurospora
109	37	59.7	795	2	Q7R178 PLAYO	Q7r178 plasmodi	182	36	58.1	664	2	Q81227 PLACH	Q81227 plasmodium
110	37	59.7	828	2	Q4KJ53 PSBFS	Q4kj53 pseudomon	183	36	58.1	695	2	Q812K2 ORYSA	Q812k2 oryza
111	37	59.7	830	2	Q9HUN7 PSBFS	Q9hun7 pseudomon	184	36	58.1	702	2	Q5P122 MIMIV	Q5p122 m.mivivus
112	37	59.7	831	2	Q4ZTW3 PSBFS	Q4ztw3 pseudomon	185	36	58.1	717	2	Q9C1F0 DROME	Q9c1f0 drosophila
113	37	59.7	955	2	Q8VTL1 PSBFS	Q8vtl1 pseudomon	186	36	58.1	726	2	Q624H3 CAEBR	Q624h3 caenorhabd
114	37	59.7	955	2	Q8S983 ORYSA	Q8s983 cryza sativ	187	36	58.1	785	2	Q8MOE6 CAEBR	Q8mo6 caenorhabd
115	37	59.7	972	2	Q4VAK4 HUMAN	Q4vak4 homo sapien	188	36	58.1	879	2	Q7RUL3 PLAYO	Q7rul3 plasmodium
116	37	59.7	972	2	Q8EV08 MYCPE	Q8ev08 mycoplasma	189	36	58.1	883	2	Q4FW40 LEIMA	Q4fw40 leishmania
117	37	59.7	1012	1	QED1 HUMAN	Qed1 homo sapien	190	36	58.1	933	2	Q5ATY7 EMENT	Q5at7 aspergillus
118	37	59.7	1197	2	Q6ZT18 HUMAN	Q6zt18 homo sapien	191	36	58.1	933	2	Q7SS83 NEUCR	Q7ss83 neurospora
119	37	59.7	1430	2	Q6V4U4 HUMAN	Q6v4u4 drosophila	192	36	58.1	1002	2	Q4H3M5 CIOIN	Q4h3m5 caryophila
120	37	59.7	1544	2	Q8X0G5 NEUCR	Q8x0g5 neurospora	193	36	58.1	1128	2	Q6NKP9 DROME	Q6nkp9 drosophila
121	37	59.7	1754	1	Q6R0G5 NEUCR	Q6r0g5 neurospora	194	36	58.1	1138	2	Q8IRJ9 DROME	Q8irj9 drosophila
122	37	59.7	1782	2	Q6R0G5 NEUCR	Q6r0g5 neurospora	195	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
123	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	196	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
124	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	197	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
125	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	198	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
126	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	199	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
127	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	200	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
128	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	201	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
129	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	202	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
130	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	203	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
131	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	204	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
132	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	205	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
133	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	206	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
134	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	207	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
135	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	208	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
136	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	209	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
137	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	210	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
138	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	211	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
139	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	212	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
140	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	213	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
141	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	214	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
142	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	215	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
143	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	216	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
144	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	217	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
145	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	218	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
146	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	219	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
147	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	220	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
148	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	221	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
149	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	222	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
150	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	223	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
151	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	224	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
152	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	225	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
153	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	226	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
154	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	227	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
155	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	228	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
156	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	229	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
157	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	230	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
158	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	231	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
159	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	232	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
160	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	233	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
161	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	234	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
162	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	235	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
163	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	236	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
164	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	237	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
165	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	238	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
166	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	239	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
167	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	240	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
168	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	241	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
169	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	242	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
170	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	243	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
171	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	244	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
172	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	245	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
173	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	246	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
174	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	247	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
175	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	248	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
176	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	249	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th
177	37	59.7	2110	2	Q5AUI7 DICI	Q5aui7 dictyostell	250	36	58.1	1180	2	Q7AL67 BACTI	Q7al67 bacillus th

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:21 ; Search time 27.1429 Seconds
(without alignments)
42.643 Million cell updates/sec

Title: US-10-067-484-1

Perfect score: 62

Sequence: 1 XXSGISNYYANPK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5.COMB.pep:*
2: /cgn2_6/prodata/1/aa/6.COMB.pep:*
3: /cgn2_6/prodata/1/aa/H.COMB.pep:*
4: /cgn2_6/prodata/1/aa/PCTUS.COMB.pep:*
5: /cgn2_6/prodata/1/aa/RS.COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	39	62.9	106	2	US-09-513-999C-8043
2	39	62.9	339	2	US-09-107-532A-3780
3	39	62.9	474	2	US-09-758-759-39
4	39	62.9	637	2	US-09-489-039A-9243
5	39	62.9	858	1	US-07-712-284-2
6	39	62.9	858	4	PCT-US92-04227-2
7	39	62.9	1024	2	US-09-091-117-5
8	38	61.3	66	2	US-09-248-796A-21394
9	38	61.3	432	2	US-09-118-319-2
10	38	61.3	432	2	US-10-070-634-2
11	37	59.7	336	2	US-09-286-591-23
12	37	59.7	336	2	US-09-687-147-23
13	37	59.7	332	2	US-09-428-034-4
14	37	59.7	376	2	US-09-428-034-2
15	37	59.7	428	2	US-09-118-319-5
16	37	59.7	515	2	US-09-107-532A-5317
17	37	59.7	700	2	US-09-620-412C-345
18	37	59.7	700	2	US-09-598-419-345
19	37	59.7	712	1	US-08-468-576B-17
20	37	59.7	712	1	US-08-468-576B-17
21	37	59.7	712	2	US-08-468-576B-17
22	37	59.7	841	2	US-08-252-991A-33134
23	37	59.7	1397	2	US-10-157-220-174
24	37	59.7	1752	2	US-09-556-877-180
25	37	59.7	1752	2	US-09-620-412C-180
26	37	59.7	1752	2	US-09-598-419-180
27	36	58.1	297	2	US-09-107-532A-5306

28	58.1	525	2	US-09-270-767-44715	Sequence 44715, A
29	58.1	1180	2	US-09-224-024-28	Sequence 28, Appl
30	58.1	1180	4	PCT-US94-07902-28	Sequence 28, Appl
31	56.5	159	2	US-09-134-000C-4250	Sequence 4250, Ap
32	56.5	247	2	US-09-248-796A-17530	Sequence 17530, A
33	56.5	247	2	US-09-270-767-32493	Sequence 32493, A
34	56.5	256	2	US-09-270-767-47710	Sequence 47710, A
35	56.5	284	2	US-09-540-236-3124	Sequence 3124, Ap
36	56.5	442	2	US-09-252-292C-29	Sequence 29, Appl
37	56.5	442	2	US-09-567-615B-8	Sequence 8, Appl
38	56.5	455	2	US-09-543-681A-8288	Sequence 8288, Ap
39	56.5	468	2	US-09-902-540-10847	Sequence 10847, A
40	56.5	870	2	US-09-543-681A-4768	Sequence 4768, Ap
41	56.5	1010	2	US-09-248-796A-16379	Sequence 16379, A
42	56.5	1545	2	US-08-296-791-4	Sequence 4, Appl
43	56.5	1545	2	US-09-839-996-4	Sequence 4, Appl
44	56.5	1545	2	US-10-080-505-4	Sequence 4, Appl
45	56.5	1545	2	US-10-645-655-4	Sequence 4, Appl
46	56.5	1545	4	PCT-US95-10661A-4	Sequence 4, Appl
47	54.8	81	2	US-09-248-796A-22138	Sequence 22138, A
48	54.8	98	2	US-09-248-796A-23711	Sequence 23711, A
49	54.8	181	2	US-09-270-767-57311	Sequence 57311, A
50	54.8	232	2	US-09-134-001C-5367	Sequence 5367, Ap
51	54.8	244	2	US-09-543-681A-7587	Sequence 7587, Ap
52	54.8	328	2	US-09-270-767-42054	Sequence 42054, A
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61	54.8	549	2	US-09-579-259-6	Sequence 6, Appl
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65	54.8	604	1	US-08-333-802-2	Sequence 2, Appl
66	54.8	605	2	US-09-147-878-46	Sequence 46, Appl
67	54.8	685	2	US-10-104-017-2916	Sequence 2916, Ap
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124	33	53.2	1367	1	US-07-906-397A-6	Sequence 6, Appl1	197	32	51.6	633	2	US-09-633-328B-3	Sequence 3, Appl1
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143	33	53.2	45	2	US-10-012-542-135	Sequence 135, App	216	32	51.6	644	2	US-10-258-842-19	Sequence 19, Appl
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150	33	53.2	173	2	US-09-540-236-2525	Sequence 2525, Ap	223	32	51.6	652	2	US-09-367-512-8	Sequence 8, Appl1
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153	33	53.2	198	2	US-09-248-796A-18306	Sequence 18306, A	226	32	51.6	662	2	US-09-198-452A-169	Sequence 169, App
154	33	53.2	198	2	US-09-107-532A-5931	Sequence 5931, App	227	32	51.6	664	1	US-08-426-125-7	Sequence 7, Appl1
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158	33	53.2	236	2	US-09-239-867-2	Sequence 2, Appl1	231	32	51.6	665	2	US-09-438-185A-151	Sequence 151, App
159	33	53.2	236	2	US-10-024-433-2	Sequence 2, Appl1	232	32	51.6	667	1	US-08-426-125-6	Sequence 6, Appl1
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163	33	53.2	257	1	US-07-857-224B-25	Sequence 25, Appl	236	32	51.6	670	1	US-09-137-478-2	Sequence 2, Appl1
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173	33	53.2	418	2	US-09-030-267-5	Sequence 5, Appl1	246	32	51.6	686	2	US-09-270-767-36547	Sequence 36547, A

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Total number of hits satisfying chosen parameters: 1867569

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	39	62.9	278	5	US-10-732-923-18495	Sequence 18495, A
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8	39	62.9	474	3	US-09-758-759-39	Sequence 39, Appl1
9	39	62.9	474	6	US-11-021-825-39	Sequence 39, Appl1
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SUMMARIES

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82	33	53.2	524	6	US-10-467-657-8258	Sequence 8258, Appl
83	33	53.2	556	7	US-11-096-568A-27991	Sequence 27991, A
84	33	53.2	594	7	US-11-096-568A-27990	Sequence 27990, A
85	33	53.2	654	7	US-10-821-334-1691	Sequence 1691, A
86	33	53.2	766	6	US-10-821-334-1691	Sequence 1691, A
87	33	53.2	960	7	US-11-169-041-177	Sequence 177, Appl
88	33	53.2	1230	7	US-11-231-599-56	Sequence 56, Appl
89	33	53.2	1343	6	US-10-541-814-15	Sequence 15, Appl
90	33	53.2	1343	6	US-10-541-814-15	Sequence 15, Appl
91	33	53.2	1678	7	US-11-124-367A-340	Sequence 340, Appl
92	33	53.2	1678	7	US-11-124-367A-341	Sequence 341, Appl
93	33	53.2	2105	7	US-11-052-554A-113	Sequence 113, Appl
94	33	53.2	386	7	US-11-079-463-7036	Sequence 7036, Appl
95	32	51.6	42	6	US-10-957-8879-53	Sequence 53, Appl
96	32	51.6	175	7	US-11-188-298-14383	Sequence 14383, A
97	32	51.6	202	7	US-11-188-298-10344	Sequence 10344, A
98	32	51.6	246	6	US-10-793-626-900	Sequence 900, Appl

99	32	51.6	246	6	US-10-793-626-1956	Sequence 1956, Ap	172	32	51.6	652	7	US-11-188-298-13868	Sequence 13868, Ap
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101	32	51.6	348	6	US-10-821-224-1614	Sequence 1174, A	174	32	51.6	655	7	US-11-079-122-13	Sequence 13, App
102	32	51.6	348	6	US-10-851-780-124	Sequence 8, App	175	32	51.6	655	7	US-11-079-122-13	Sequence 15, App
103	32	51.6	348	7	US-11-108-088-28	Sequence 65, App	176	32	51.6	655	7	US-11-188-298-21509	Sequence 25, App
104	32	51.6	348	7	US-11-108-088-28	Sequence 65, App	177	32	51.6	655	7	US-11-076-733-25	Sequence 22, App
105	32	51.6	348	7	US-11-108-088-28	Sequence 156, App	178	32	51.6	656	7	US-11-198-728-22	Sequence 24, App
106	32	51.6	348	7	US-11-087-039-6389	Sequence 8389, Ap	179	32	51.6	656	7	US-11-149-420-24	Sequence 22, App
107	32	51.6	348	7	US-11-149-349-4	Sequence 4, App	180	32	51.6	656	7	US-11-188-298-14470	Sequence 14470, Ap
108	32	51.6	446	7	US-11-188-298-13393	Sequence 13393, A	181	32	51.6	658	7	US-11-188-298-14610	Sequence 14610, Ap
109	32	51.6	446	7	US-11-079-463-6726	Sequence 6726, Ap	182	32	51.6	659	7	US-11-188-298-14156	Sequence 14156, Ap
110	32	51.6	446	7	US-11-188-298-11562	Sequence 11655, A	183	32	51.6	659	7	US-11-188-298-14182	Sequence 21282, A
111	32	51.6	468	7	US-11-188-298-12494	Sequence 12494, A	184	32	51.6	659	7	US-11-188-298-21603	Sequence 21603, A
112	32	51.6	468	7	US-11-188-298-15633	Sequence 15633, A	185	32	51.6	659	7	US-11-188-298-15639	Sequence 16359, A
113	32	51.6	468	7	US-11-188-298-11810	Sequence 11810, A	186	32	51.6	662	7	US-11-188-298-15458	Sequence 15458, Ap
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115	32	51.6	472	7	US-11-188-298-11065	Sequence 11065, A	188	32	51.6	664	7	US-11-188-298-908	Sequence 908, App
116	32	51.6	482	6	US-10-793-626-24	Sequence 24, App	189	32	51.6	664	7	US-11-188-298-21482	Sequence 21482, Ap
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119	32	51.6	521	7	US-11-188-298-6909	Sequence 6909, Ap	192	32	51.6	667	7	US-11-188-298-14182	Sequence 14182, A
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123	32	51.6	567	7	US-11-188-298-10168	Sequence 10167, A	196	32	51.6	668	7	US-11-188-298-121795	Sequence 21795, A
124	32	51.6	567	7	US-11-188-298-18477	Sequence 18477, A	197	32	51.6	669	7	US-11-188-298-4171	Sequence 4171, Ap
125	32	51.6	575	7	US-11-188-298-9567	Sequence 9567, Ap	198	32	51.6	669	7	US-11-188-298-13639	Sequence 13639, Ap
126	32	51.6	577	7	US-11-188-298-15593	Sequence 15593, Ap	199	32	51.6	670	7	US-11-188-298-9996	Sequence 9996, Ap
127	32	51.6	583	7	US-11-188-298-797	Sequence 795, App	200	32	51.6	670	7	US-11-188-298-17459	Sequence 17459, A
128	32	51.6	583	7	US-11-188-298-4277	Sequence 4277, Ap	201	32	51.6	670	7	US-11-188-298-18745	Sequence 18745, A
129	32	51.6	585	7	US-11-188-298-3313	Sequence 3313, Ap	202	32	51.6	670	7	US-11-188-298-18745	Sequence 21602, A
130	32	51.6	585	7	US-11-188-298-7344	Sequence 3744, Ap	203	32	51.6	670	7	US-11-188-298-121602	Sequence 121602, A
131	32	51.6	585	7	US-11-188-298-5911	Sequence 5911, Ap	204	32	51.6	686	7	US-11-065-943-52	Sequence 52, App
132	32	51.6	585	7	US-11-188-298-8243	Sequence 8243, Ap	205	32	51.6	686	7	US-11-188-298-1307	Sequence 1307, Ap
133	32	51.6	585	7	US-11-188-298-9599	Sequence 9599, Ap	206	32	51.6	686	7	US-11-188-298-7370	Sequence 7370, Ap
134	32	51.6	585	7	US-11-188-298-10486	Sequence 10486, Ap	207	32	51.6	686	7	US-11-188-298-9628	Sequence 9628, Ap
135	32	51.6	585	7	US-11-188-298-15561	Sequence 15561, A	208	32	51.6	686	7	US-11-188-298-9628	Sequence 10425, A
136	32	51.6	585	7	US-11-188-298-17836	Sequence 17836, A	209	32	51.6	686	7	US-11-188-298-11072	Sequence 11072, A
137	32	51.6	585	7	US-11-188-298-19452	Sequence 19452, A	210	32	51.6	686	7	US-11-188-298-11346	Sequence 11346, A
138	32	51.6	585	7	US-11-188-298-40104	Sequence 20104, A	211	32	51.6	686	7	US-11-188-298-11525	Sequence 11525, A
139	32	51.6	585	7	US-11-188-298-22371	Sequence 22371, A	212	32	51.6	686	7	US-11-188-298-15238	Sequence 15238, Ap
140	32	51.6	586	7	US-11-152-903-4	Sequence 2, App	213	32	51.6	713	7	US-11-188-298-7230	Sequence 7230, Ap
141	32	51.6	586	7	US-11-152-903-6	Sequence 6, App	214	32	51.6	713	7	US-11-188-298-8280	Sequence 8280, Ap
142	32	51.6	586	7	US-11-152-903-6	Sequence 6, App	215	32	51.6	713	7	US-11-188-298-14307	Sequence 14307, A
143	32	51.6	586	7	US-11-152-903-6	Sequence 6, App	216	32	51.6	713	7	US-11-188-298-15629	Sequence 15629, A
144	32	51.6	586	7	US-11-152-903-12	Sequence 12, App	217	32	51.6	713	7	US-11-188-298-15629	Sequence 15629, A
145	32	51.6	586	7	US-11-152-903-12	Sequence 12, App	218	32	51.6	718	7	US-11-188-298-609	Sequence 609, App
146	32	51.6	586	7	US-11-188-298-1244	Sequence 1244, Ap	219	32	51.6	718	7	US-11-188-298-7034	Sequence 7034, App
147	32	51.6	586	7	US-11-188-298-12610	Sequence 12610, Ap	220	32	51.6	718	7	US-11-188-298-7034	Sequence 7034, App
148	32	51.6	586	7	US-11-188-298-13894	Sequence 13894, A	221	32	51.6	718	7	US-11-188-298-18127	Sequence 18127, Ap
149	32	51.6	586	7	US-11-188-298-22524	Sequence 22524, Ap	222	32	51.6	718	7	US-11-079-463-5761	Sequence 5761, Ap
150	32	51.6	586	7	US-11-188-298-15409	Sequence 15409, A	223	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
151	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	224	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
152	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	225	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
153	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	226	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
154	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	227	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
155	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	228	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
156	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	229	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
157	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	230	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
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159	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	232	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
160	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	233	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
161	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	234	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
162	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	235	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
163	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	236	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
164	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	237	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
165	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	238	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
166	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	239	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
167	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	240	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
168	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	241	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
169	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	242	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
170	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	243	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A
171	32	51.6	586	7	US-11-087-039-8358	Sequence 8358, Ap	244	32	51.6	1216	7	US-11-096-5688-28970	Sequence 28970, A

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:40:47 ; Search time 90.7347 Seconds
(without alignments)
43.582 Million cell updates/sec

Title: US-10-067-484-2
Perfect score: 42
Sequence: 1 PRSMXATK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	97.6	9	5	ABH81969 30 kDa ra
2	34	81.0	424	6	ABU41254 Protein e
3	33	78.6	135	3	AAAB24649 Plant SDF
4	33	78.6	271	3	AAAG10010 Arabidops
5	33	78.6	345	4	ABAB60198 Drosophila
6	32	76.2	158	8	ADK78345 Plant ful
7	32	76.2	232	7	ABOC60780 Klebsiell
8	32	76.2	360	4	AAW41900 Human pol
9	32	76.2	663	4	ABAB52462 Escherich
10	32	76.2	713	7	ADCO1362 Enteroha
11	32	76.2	713	9	AEAB91364 Microbia
12	32	76.2	808	7	ADJ68916 Human hea
13	32	76.2	2194	4	AAW40114 Human pol
14	32	76.2	2829	8	ADL72180 X. laevis
15	31	73.8	110	4	AAAB62783 Human HIV
16	31	73.8	126	4	ABG02725 Novel hum
17	31	73.8	457	4	ABAB69700 Drosophila
18	31	73.8	1361	6	ABU20358 Protein e
19	31	73.8	6815	4	ABAB6811 Drosophila
20	30	71.4	85	1	AAW70412 ORF 9 gen
21	30	71.4	100	2	AAW35084 Chlamydia
22	30	71.4	110	6	ABP60080 Mouse RGS
23	30	71.4	154	7	ABO65493 Klebsiell
24	30	71.4	187	4	ABG04966 Novel hum

25	30	71.4	214	7	ADH86644 Enterococ
26	30	71.4	287	7	ABO74345 Pseudomon
27	30	71.4	319	4	AAU63426 Propionib
28	30	71.4	319	6	ABW65512 Propionib
29	30	71.4	319	6	ABW65512 Propionib
30	30	71.4	319	6	ABW65512 Propionib
31	30	71.4	407	8	ADN24100 Bacterial
32	30	71.4	418	5	ABAB69699 Canine AS
33	30	71.4	426	6	ABP77795 N. gonorr
34	30	71.4	426	6	ABP77795 N. gonorr
35	30	71.4	441	6	ADJ35082 Actinocob
36	30	71.4	441	6	ADJ35082 Actinocob
37	30	71.4	851	8	ADQ66949 Novel hum
38	30	71.4	870	2	AAW31348 Jaagsiek
39	30	71.4	987	8	ADL05331 M. catarr
40	30	71.4	1362	6	ABU17069 Protein e
41	30	71.4	1363	6	ABU35175 Protein e
42	30	71.4	1380	6	ADJ35082 Actinocob
43	30	71.4	2626	3	ADJ35082 Actinocob
44	29	69.0	65	6	ABW7569 Protein e
45	29	69.0	65	6	ABW7569 Protein e
46	29	69.0	106	2	AAW71241 Propionib
47	29	69.0	107	9	AEAA8156 Mouse ant
48	29	69.0	107	9	AEAA8156 Mouse ant
49	29	69.0	107	9	AEAA8156 Mouse ant
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54	29	69.0	107	9	AEAA8156 Mouse ant
55	29	69.0	112	7	ADD13784 Kappa ex
56	29	69.0	127	2	AAW08945 Kappa lig
57	29	69.0	127	2	AAW08941 Kappa lig
58	29	69.0	127	2	AAW08943 Kappa lig
59	29	69.0	178	6	ABR33685 Protein e
60	29	69.0	178	7	ADK64062 Lactococ
61	29	69.0	202	5	ABR55266 Lactococ
62	29	69.0	214	9	AEAA8166 Mouse ant
63	29	69.0	214	9	AEAA8166 Mouse ant
64	29	69.0	233	6	ABU44004 Protein e
65	29	69.0	233	6	ADU14301 EGFR lig
66	29	69.0	236	8	ADP44635 Murine an
67	29	69.0	236	8	AEAA6461 Fv(TU25)
68	29	69.0	239	2	AAW05133 Single ch
69	29	69.0	240	2	AAW71243 scFv comp
70	29	69.0	240	2	AAW71243 scFv comp
71	29	69.0	292	6	ADJ34980 Actinocob
72	29	69.0	296	6	ADK88689 Plant ful
73	29	69.0	340	5	ABP40337 Staphyloc
74	29	69.0	340	8	ADSO4889 Staphyloc
75	29	69.0	413	6	ABU22839 Protein e
76	29	69.0	417	8	ADJ45281 Rice isop
77	29	69.0	487	5	AAU76889 Pneumococ
78	29	69.0	494	4	AAU76889 Pneumococ
79	29	69.0	494	6	ABU14759 Protein e
80	29	69.0	498	7	ADU13794 Plasmid p
81	29	69.0	500	7	ADU13792 Plasmid p
82	29	69.0	651	2	AAW05135 scFv(225)
83	29	69.0	722	6	ABU27630 Protein e
84	29	69.0	754	8	ADN25644 Bacterial
85	29	69.0	784	8	ADN25644 Bacterial
86	29	69.0	785	9	ABW90808 M. xanthu
87	29	69.0	892	2	AAW05140 scFv2(225)
88	29	69.0	892	2	AAW05139 scFv2(FRP
89	29	69.0	913	8	ADN24100 Bacterial
90	29	69.0	924	8	ADN21843 Bacterial
91	29	69.0	935	7	ADN21843 Bacterial
92	29	69.0	946	8	ADN25957 Bacterial
93	29	69.0	1001	6	ABU21679 Protein e
94	29	69.0	1042	2	AAW05141 scFv2(FRP
95	29	69.0	1060	6	ABU22137 Protein e
96	29	69.0	1060	6	ABU22137 Protein e
97	29	69.0	1172	4	ABW64804 Drosophila

98	29	69.0	1514	2	AAW37390	Mouse add
99	29	69.0	1514	2	AAW37392	Mouse add
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101	28	66.7	32	2	AAW60354	Human not
102	28	66.7	34	3	AAW68521	Human not
103	28	66.7	34	3	AAW68513	Consensus
104	28	66.7	34	3	AAW68506	Consensus
105	28	66.7	34	3	AAW68512	Consensus
106	28	66.7	34	3	AAW68520	Consensus
107	28	66.7	34	3	AAW68507	Consensus
108	28	66.7	34	3	AAW68511	Consensus
109	28	66.7	36	3	AAW68510	Consensus
110	28	66.7	36	3	AAW68505	Consensus
111	28	66.7	36	3	AAW68507	Consensus
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115	28	66.7	57	3	AAW68531	Consensus
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138	28	66.7	84	3	AAW68531	Consensus
139	28	66.7	84	3	AAW68531	Consensus
140	28	66.7	84	3	AAW68531	Consensus
141	28	66.7	84	3	AAW68531	Consensus
142	28	66.7	84	3	AAW68531	Consensus
143	28	66.7	84	3	AAW68531	Consensus
144	28	66.7	84	3	AAW68531	Consensus
145	28	66.7	84	3	AAW68531	Consensus
146	28	66.7	84	3	AAW68531	Consensus
147	28	66.7	84	3	AAW68531	Consensus
148	28	66.7	84	3	AAW68531	Consensus
149	28	66.7	84	3	AAW68531	Consensus
150	28	66.7	84	3	AAW68531	Consensus
151	28	66.7	84	3	AAW68531	Consensus
152	28	66.7	84	3	AAW68531	Consensus
153	28	66.7	84	3	AAW68531	Consensus
154	28	66.7	84	3	AAW68531	Consensus
155	28	66.7	84	3	AAW68531	Consensus
156	28	66.7	84	3	AAW68531	Consensus
157	28	66.7	84	3	AAW68531	Consensus
158	28	66.7	84	3	AAW68531	Consensus
159	28	66.7	84	3	AAW68531	Consensus
160	28	66.7	84	3	AAW68531	Consensus
161	28	66.7	84	3	AAW68531	Consensus
162	28	66.7	84	3	AAW68531	Consensus
163	28	66.7	84	3	AAW68531	Consensus
164	28	66.7	84	3	AAW68531	Consensus

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OW protein - protein search, using sw model

Run on: April 18, 2006, 10:41:12 ; Search time 8.26531 Seconds
(without alignments)
104.769 Million cell updates/sec

Title: US-10-067-484-2
Perfect score: 42
Sequence: 1 PTSPNXXRK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	35	83.3	336	2 T09133	heat shock protein
2	33	78.6	345	2 B43731	achete-scute comp
3	33	78.6	605	2 S18648	protein kinase wis
4	33	78.6	779	1 MMVZAL	ribonucleoside-dip
5	32	76.2	405	2 A75105	hypothetical prote
6	32	76.2	713	2 B91118	probable ferrichro
7	32	76.2	713	2 D85963	probable iron comp
8	31	73.8	127	2 T395086	hypothetical prote
9	31	73.8	372	2 T39649	cell division cont
10	31	73.8	1300	2 T18364	ro-3 protein - Neu
11	31	73.8	1347	2 T41321	BTB domain and Ank
12	30	71.4	307	2 G69501	UDP-glucose 4-epim
13	30	71.4	362	2 A10433	trypsin-like prote
14	30	71.4	371	2 T16391	hypothetical prote
15	30	71.4	399	2 AD2559	hypothetical prote
16	30	71.4	407	2 B81914	probable transmemb
17	30	71.4	414	2 C89428	protein T08D2.7 [l
18	30	71.4	426	2 F81187	glucose/galactose
19	30	71.4	498	2 H97214	endoglucanase, fam
20	30	71.4	529	2 AH0453	bidirectional purin
21	30	71.4	638	2 AE1483	B. subtilis IOD P
22	30	71.4	687	2 D84126	penicillin-binding
23	30	71.4	870	1 GNMVJA	pol polyprotein -
24	30	71.4	1029	2 H86179	hypothetical prote
25	29	69.0	178	2 S51388	hypothetical prote
26	29	69.0	202	2 A86864	conserved hypothet
27	29	69.0	213	2 A87259	hypothetical prote
28	29	69.0	216	2 AH2635	bacteriophage repr
29	29	69.0	216	2 G97417	hypothetical prote

30	29	69.0	256	2 C90443	hypothetical prote
31	29	69.0	374	2 S53829	ribosomal protein
32	29	69.0	389	2 S68175	cone arrestin - bu
33	29	69.0	389	2 S68172	cone arrestin - no
34	29	69.0	470	2 T5196	hypothetical prote
35	29	69.0	480	2 B64308	hypothetical prote
36	29	69.0	494	2 D64944	probable permease
37	29	69.0	494	2 F85794	probable transport
38	29	69.0	494	2 B90946	probable transport
39	29	69.0	498	1 HJBE11	helicase (EC 3.6.1
40	29	69.0	523	2 T50478	neuroilin - goldfif
41	29	69.0	527	2 D87318	conserved hypothet
42	29	69.0	743	2 T42557	regument protein 1
43	29	69.0	903	2 J80327	dynamn-related pr
44	29	69.0	903	2 T50334	dynamn-related pr
45	29	69.0	1350	2 T10803	probable RNA-direc
46	28	66.7	77	2 T14930	hypothetical prote
47	28	66.7	88	2 T30366	occlusion-derived
48	28	66.7	108	2 K1H0HU	Ig kappa chain V-I
49	28	66.7	109	2 S61253	genome polypotein
50	28	66.7	109	2 S61252	genome polypotein
51	28	66.7	109	2 S61255	genome polypotein
52	28	66.7	110	2 S61257	genome polypotein
53	28	66.7	110	2 S61254	genome polypotein
54	28	66.7	121	2 S40371	Ig kappa chain - h
55	28	66.7	128	2 PN0445	Ig kappa chain pre
56	28	66.7	137	2 S35916	capsid protein VP1
57	28	66.7	137	2 A95297	hypothetical prote
58	28	66.7	201	2 S75047	dirga protein - Syn
59	28	66.7	202	2 E97130	uncharacterized se
60	28	66.7	203	2 G81700	thymidylate kinase
61	28	66.7	203	2 JCI335	genome polypotein
62	28	66.7	209	2 JCI329	genome polypotein
63	28	66.7	209	2 JCI332	genome polypotein
64	28	66.7	209	2 JCI333	genome polypotein
65	28	66.7	209	2 JCI331	genome polypotein
66	28	66.7	209	2 JCI330	genome polypotein
67	28	66.7	209	2 JCI334	genome polypotein
68	28	66.7	209	2 JCI328	genome polypotein
69	28	66.7	213	2 S35917	capsid protein VP1
70	28	66.7	234	2 A03912	genome polypotein
71	28	66.7	247	2 P00661	outer capsid spike
72	28	66.7	247	2 P00659	outer capsid spike
73	28	66.7	265	2 JH0300	synaptoporin - rat
74	28	66.7	274	1 I52851	NAD(P)H2 dehydroge
75	28	66.7	274	1 A30879	NAD(P)H2 dehydroge
76	28	66.7	274	1 A34162	NAD(P)H2 dehydroge
77	28	66.7	274	1 A57691	NAD(P)H2 dehydroge
78	28	66.7	281	1 VPRRRR	NAD(P)H2 dehydroge
79	28	66.7	299	2 A45720	outer capsid prote
80	28	66.7	309	2 S73869	P35 orf135 - Bomby
81	28	66.7	332	2 A03913	hypothetical prote
82	28	66.7	340	2 A35009	genome polypotein
83	28	66.7	341	2 G84588	hypothetical prote
84	28	66.7	342	2 S63654	C 3.4.23.42 therno
85	28	66.7	354	1 G64648	hypothetical prote
86	28	66.7	354	2 G71938	hypothetical prote
87	28	66.7	359	2 H81421	flagellar motor SW
88	28	66.7	359	2 T01049	flagellar motor SW
89	28	66.7	400	2 T19517	flagellar motor SW
90	28	66.7	409	1 BVBSCB	hypothetical prote
91	28	66.7	428	2 S48836	competence protein
92	28	66.7	428	2 B75133	cytochrome-c3 hydr
93	28	66.7	429	2 C71075	cytochrome-c3 hydr
94	28	66.7	431	2 T02064	probable cytochrom
95	28	66.7	434	2 AG1697	histone acetyltran
96	28	66.7	465	2 S61133	hypothetical prote
97	28	66.7	471	2 G75627	probable membrane
98	28	66.7	512	2 AB0603	hypothetical prote
99	28	66.7	520	2 B75332	probable ABC trans
100	28	66.7	521	2 T05684	extracellular solu
101	28	66.7	524	2 S55097	hypothetical prote
102	28	66.7	561	2 G90328	probable membrane

103	28	66.7	584	2	D81265	hypothetical prote
104	28	66.7	585	2	S46034	hypothetical prote
105	28	66.7	609	2	T28896	hypothetical prote
106	28	66.7	624	2	S27962	modulator recognit
107	28	66.7	643	2	A43647	parasporel crystal
108	28	66.7	645	2	A82689	DNA helicase Xf138
109	28	66.7	648	2	A32576	beta-glucuronidase
110	28	66.7	648	2	A25047	beta-glucuronidase
111	28	66.7	733	2	JQ1891	capaid protein - 4
112	28	66.7	733	2	JQ1892	capaid protein - 4
113	28	66.7	747	2	ORECFE	ferrichrome-iron x
114	28	66.7	747	2	B85499	outer membrane rec
115	28	66.7	747	2	B90648	outer membrane rec
116	28	66.7	776	2	VPXRHH	outer layer protei
117	28	66.7	776	2	A48731	outer layer protei
118	28	66.7	841	2	S69563	suppressor protein
119	28	66.7	993	2	E86245	hypothetical prote
120	28	66.7	1011	2	T09129	probable erythrocy
121	28	66.7	1011	2	GNNYCI	genome polyprotein
122	28	66.7	1075	2	S54067	probable membrane
123	28	66.7	1643	2	RRMGNV	genome polyprotein
124	28	66.7	1901	2	T09127	probable erythrocy
125	28	66.7	1901	2	AQ2391	berline/rheumatoec
126	28	66.7	1978	2	S71257	hypothetical prote
127	28	66.7	2014	2	T21560	hypothetical prote
128	28	66.7	2149	2	C36695	ribulose biphosph
129	28	66.7	2332	1	GNNYF	genome polyprotein
130	28	66.7	2336	2	S37077	genome polyprotein
131	28	66.7	2405	2	T81614	transcription fact
132	28	66.7	2539	2	A56923	transcription fact
133	28	66.7	2561	2	T24864	hypothetical prote
134	28	66.7	2578	2	A56046	transcription fact
135	27	64.3	115	2	T40621	hypothetical prote
136	27	64.3	115	2	C81142	hypothetical prote
137	27	64.3	142	1	S61539	hypothetical prote
138	27	64.3	142	1	S61539	hypothetical prote
139	27	64.3	142	1	S61539	hypothetical prote
140	27	64.3	219	2	H17585	interleukin-3 prec
141	27	64.3	219	2	S14242	hydrogenase expres
142	27	64.3	219	2	S14242	hydrogenase expres
143	27	64.3	219	2	S03766	targeted effector
144	27	64.3	222	2	H97300	hypothetical protei
145	27	64.3	222	2	H97300	hypothetical protei
146	27	64.3	223	2	H64098	hypothetical protei
147	27	64.3	223	2	H64098	hypothetical protei
148	27	64.3	223	2	H64098	hypothetical protei
149	27	64.3	223	2	H64098	hypothetical protei
150	27	64.3	223	2	H64098	hypothetical protei
151	27	64.3	223	2	H64098	hypothetical protei
152	27	64.3	223	2	H64098	hypothetical protei
153	27	64.3	223	2	H64098	hypothetical protei
154	27	64.3	223	2	H64098	hypothetical protei
155	27	64.3	223	2	H64098	hypothetical protei
156	27	64.3	223	2	H64098	hypothetical protei
157	27	64.3	223	2	H64098	hypothetical protei
158	27	64.3	223	2	H64098	hypothetical protei
159	27	64.3	223	2	H64098	hypothetical protei
160	27	64.3	223	2	H64098	hypothetical protei
161	27	64.3	223	2	H64098	hypothetical protei
162	27	64.3	223	2	H64098	hypothetical protei
163	27	64.3	223	2	H64098	hypothetical protei
164	27	64.3	223	2	H64098	hypothetical protei
165	27	64.3	223	2	H64098	hypothetical protei
166	27	64.3	223	2	H64098	hypothetical protei
167	27	64.3	223	2	H64098	hypothetical protei
168	27	64.3	223	2	H64098	hypothetical protei
169	27	64.3	223	2	H64098	hypothetical protei
170	27	64.3	223	2	H64098	hypothetical protei
171	27	64.3	223	2	H64098	hypothetical protei
172	27	64.3	223	2	H64098	hypothetical protei
173	27	64.3	223	2	H64098	hypothetical protei
174	27	64.3	223	2	H64098	hypothetical protei
175	27	64.3	223	2	H64098	hypothetical protei

probable sugar tra
glutathione-indupe
chitinase - fungus
chitinase I precu
probable solute-bi
probable ABC transp
nucleoporin lumen-bi
probable solute-bi
Na+/H+ exchanger
membrane nucleoside
probable ABC precuro
peptidase M20/M25
unknown protein P1
probable transport A
ribotase (RC 1.11.
catalase zinc fing
probable N1L prote
probable pectinest
pectinesterase (BC
1 cell activation
hypothetical prote
hypothetical pectinest
P22D16.20 protein
hypothetical prote
hypothetical prote
hypothetical prote
probable protein X
SACT protein - yea
hypothetical prote
probable zinc fing
V-type ATP synthas
hypothetical prote
stomatocxin beta c
cyclonucleoside-dip
ribonucleoside-dip
ribonucleoside-dip
ribonucleoside-dip
ribonucleoside-dip
L4L protein - Vari
outer layer protei
cell division cont
ribonucleoside-dip
ribonucleoside-dip
ribonucleoside-dip
hypothetical prote
ribonucleoside-dip
ribonucleoside-dip
ribonucleoside-dip
ribonucleoside-dip
hypothetical prote
probable secreted
ribonucleoside-dip
hypothetical prote
conserved hypotet
ribonucleoside-dip
ribonucleoside-dip
cell wall surface
ribonucleoside-dip
ribonucleoside-dip
ribonucleoside-dip
ribonucleoside-dip
fibronectin-bindin
Tomb-dependent rec
hypothetical prote
probable membrane
hypothetical prote
hypothetical prote
X-linked nuclear p

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:05 ; Search time 49.0408 Seconds
(without alignments)
129.479 Million cell updates/sec

Title: US-10-067-484-2
Perfect score: 42
Sequence: 1 PTFPMXARK 9

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	83.3	336	076224	GYRYP 076224 trypanosoma
2	35	83.3	492	081NH2	BACAN 081nh2 bacillus an
3	34	81.0	398	082MX5	PYRAE 082mx5 pyrobaculum
4	34	81.0	434	0893V9	CLOTE 0893v9 clostridium
5	33	78.6	178	060Y71	CABER 060y71 caenorhabdi
6	33	78.6	242	08KDZ1	CHLRE 08kdz1 chlorobium
7	33	78.6	250	0517R9	ENTHI 0517r9 entamoeba h
8	33	78.6	271	0941A9	ARATH 0941a9 arabidopsis
9	33	78.6	336	077029	DROYA 077029 drosophila
10	33	78.6	345	1AST4	DROME 1ast4 drosophila
11	33	78.6	345	04V705	DROME 04v705 drosophila
12	33	78.6	346	077031	DROSI 077031 drosophila
13	33	78.6	460	06C3D8	YARLI 06c3d8 yarrowia li
14	33	78.6	468	0758Z1	ASHGO 0758z1 ashyia goss
15	33	78.6	605	1WIS1	SCHPO 1wis1 schizosacch
16	33	78.6	778	1RIR1	ASFB7 1rir1 asf7
17	33	78.6	779	1RIR1	ASFB7 1rir1 asf7
18	33	78.6	901	06CAJ2	YARLI 06caj2 yarrowia li
19	33	78.6	1041	06XST7	STREU 06xst7 streptococ
20	32	76.2	104	05Z7J8	ORISA 05z7j8 oryza sativ
21	32	76.2	185	09AT89	ORISA 09at89 oryza sativ
22	32	76.2	185	05FNM5	GLUXO 05fnm5 gluconobact
23	32	76.2	311	054QD9	DICDI 054qd9 dictyostell
24	32	76.2	320	07RGP9	PLAYO 07rgp9 plasmodium
25	32	76.2	388	04XW08	PLACH 04xw08 plasmodium
26	32	76.2	405	09UZB7	PYRAB 09uzb7 pyrococcus
27	32	76.2	459	05LDS1	BACRN 05lds1 bacteroides
28	32	76.2	459	064U70	BACFR 064u70 bacteroides
29	32	76.2	468	04Z327	PLABE 04z327 plasmodium
30	32	76.2	492	04MXD6	BACCE 04mxd6 bacillus ce
31	32	76.2	492	0735B2	BACCI 0735b2 bacillus ce

32	32	76.2	492	2	06HGM1	BACHK 06hgm1 bacillus th
33	32	76.2	492	2	0639A8	BACCZ 0639a8 bacillus ce
34	32	76.2	521	2	04LINO	JBURK 04lino burkholderi
35	32	76.2	713	2	08PDI8	ECOL6 08pdi8 escherichia
36	32	76.2	713	2	08XB05	ECOS7 08xb05 escherichia
37	32	76.2	808	2	09UK88	HUMAN 09uk88 homo sapien
38	32	76.2	844	2	06P517	HUMAN 06p517 homo sapien
39	32	76.2	881	2	05RBE3	PONPY 05rbe3 pongo pygma
40	32	76.2	891	2	04UBQ2	THEAN 04ubq2 theileria a
41	32	76.2	897	2	06FL60	CANCA 06fl60 candida gla
42	32	76.2	1378	2	05G4U4	GYRYP 05g4u4 trypanosoma
43	32	76.2	1434	2	08LJ13	PLAF7 08lj13 plasmodium
44	32	76.2	1636	2	04TBC0	TESTG 04tbc0 tetraodon n
45	32	76.2	1646	2	05CFZ6	CRYHO 05cfz6 cryptospori
46	32	76.2	1940	2	07SAX4	NEURC 07sax4 neurospora
47	32	76.2	2829	1	APC	XENLA APC xenla
48	32	76.2	3347	2	08MMJ9	BOMMO 08mmj9 bombyx mori
49	32	76.2	3354	2	08T101	BOMMO 08t101 bombyx mori
50	31	73.8	88	2	08JUI4	GPICO 08jui4 foot -and-mo
51	31	73.8	124	2	0949J0	CUCSA 0949j0 cucumis sat
52	31	73.8	124	2	09UZR0	PYRAB 09uzr0 pyrococcus
53	31	73.8	130	2	04ZWH5	PESRY 04zwh5 pseudomonas
54	31	73.8	130	2	04LBB8	PESRH 04lbb8 pseudomonas
55	31	73.8	133	2	06PUC2	ANOGA 06puc2 anopheles g
56	31	73.8	135	2	08BCV7	PSEBK 08bcv7 pseudomonas
57	31	73.8	156	2	06F173	MESFL 06f173 mesoplasma
58	31	73.8	190	2	05DQ15	PRILI 05dq15 asplenium o
59	31	73.8	193	2	05DQ19	PRILI 05dq19 asplenium t
60	31	73.8	195	2	05DQ08	PRILI 05dq08 asplenium t
61	31	73.8	211	2	0952X8	PTULM 0952x8 patula tae
62	31	73.8	211	2	0952Y3	PTULM 0952y3 patula moo
63	31	73.8	211	2	0952Y4	PTULM 0952y4 patula moo
64	31	73.8	211	2	0952X5	PTULM 0952x5 patula loh
65	31	73.8	221	2	0872B6	NEURC 0872b6 neurospora
66	31	73.8	241	2	06UHA0	CABER 06uha0 caenorhabdi
67	31	73.8	252	2	05Z6U8	MAGFR 05z6u8 magnaporthe
68	31	73.8	262	2	08DLX3	SYNBL 08dlx3 syntropho
69	31	73.8	267	2	07VUP4	HELHP 07vup4 helicobacte
70	31	73.8	287	2	051B19	ENTHI 051b19 entamoeba h
71	31	73.8	294	2	0981B7	RHIZO 0981b7 rhizobium l
72	31	73.8	310	2	06D9X6	ERWCT 06d9x6 erynia car
73	31	73.8	359	2	08XIV3	CLOPE 08xiv3 clostridium
74	31	73.8	372	1	DPD03	SCHPO 1dpd03 schizosacch
75	31	73.8	388	2	08A308	BACTN 08a308 bacteroides
76	31	73.8	397	2	08TFB0	TRIVE 08tfb0 trichoderma
77	31	73.8	425	2	05Z4G8	MAGFR 05z4g8 magnaporthe
78	31	73.8	457	2	09VGU7	DROME 09vgu7 drosophila
79	31	73.8	474	2	07PZT6	ANOGA 07pzt6 anopheles g
80	31	73.8	498	2	09FT67	ARATH 09ft67 arabidopsis
81	31	73.8	525	2	05XEP8	ARATH 05xep8 arabidopsis
82	31	73.8	525	2	08LPJ6	ARATH 08lpj6 arabidopsis
83	31	73.8	540	2	04VBB5	RAT 04vbb5 rattus norv
84	31	73.8	633	2	06CHX2	YARLI 06chx2 yarrowia li
85	31	73.8	658	2	04KFL8	PSEBF 04kfl8 pseudomonas
86	31	73.8	726	2	051C30	ENTHI 051c30 entamoeba h
87	31	73.8	790	2	0891X1	CLOTE 0891x1 clostridium
88	31	73.8	791	2	06CH93	YARLI 06ch93 yarrowia li
89	31	73.8	1130	2	08EMB7	MYCPE 08emb7 mycoplasma
90	31	73.8	1300	1	DYNA	NEURC 1dyna neurospora
91	31	73.8	1328	2	064XZ1	BACFR 064xz1 bacteroides
92	31	73.8	1447	2	0748B1	SCHPO 0748b1 schizosacch
93	31	73.8	1361	2	05LH34	BACFN 05lh34 bacteroides
94	31	73.8	1504	2	051TP6	MAGFR 051tp6 magnaporthe
95	31	73.8	1704	2	054V07	DICDI 054v07 dictyostell
96	31	73.8	1836	2	04WHH4	ASFPV 04whh4 aspergillus
97	31	73.8	3340	2	04QBB2	LEITMA 04qbb2 leishmania
98	31	73.8	16215	2	09NFS3	DROME 09nfs3 drosophila
99	31	73.8	17903	2	07RTL4	DROME 07rtl4 drosophila
100	31	73.8	18074	2	091TU4	DROME 091tu4 drosophila
101	30.5	72.6	45	2	091HS1	GPICO 091hs1 foot -and-mo
102	30.5	72.6	55	2	09DSB0	GPICO 09dsb0 foot -and-mo
103	30.5	72.6	77	2	091H65	GPICO 091h65 foot -and-mo
104	30.5	72.6	81	2	091H50	GPICO 091h50 foot -and-mo

06hgm1	bacillus th
0639a8	bacillus ce
04lino	burkholderi
08pdi8	ecol6
08xb05	eschrichia
09uk88	homo sapien
06p517	homo sapien
05rbe3	pongo pygma
04ubq2	theileria a
06fl60	candida gla
05g4u4	trypanosoma
08lj13	plasmodium
04tbc0	tetraodon n
05cfz6	cryptospori
07sax4	neurospora
P70039	xenopus lae
08mmj9	bombyx mori
08t101	bombyx mori
08jui4	foot -and-mo
0949j0	cucumis sat
09uzr0	pyrococcus
04zwh5	pseudomonas
04lbb8	pseudomonas
06puc2	anopheles g
08bcv7	pseudomonas
06f173	mesoplasma
05dq15	asplenium o
05dq19	asplenium t
05dq08	asplenium t
0952x8	patula tae
0952y3	patula moo
0952y4	patula moo
0952x5	patula loh
0872b6	neurospora
06uha0	caenorhabdi
05z6u8	magnaporthe
08dlx3	syntropho
07vup4	helicobacte
051b19	entamoeba h
0981b7	rhizobium l
06d9x6	erynia car
08xiv3	clostridium
P30261	schizosacch
08a308	bacteroides
08tfb0	trichoderma
05z4g8	magnaporthe
09vgu7	drosophila
07pzt6	anopheles g
09ft67	arabidopsis
05xep8	arabidopsis
08lpj6	arabidopsis
04vbb5	rattus norv
06chx2	yarrowia li
04kfl8	pseudomonas
051c30	entamoeba h
0891x1	clostridium
06ch93	yarrowia li
08emb7	mycoplasma
001397	neurospora
064xz1	bacteroides
0748b1	schizosacch
05lh34	bacteroides
051tp6	magnaporthe
054v07	dictyostell
04whh4	aspergillus
04qbb2	leishmania
09nfs3	drosophila
07rtl4	drosophila
091tu4	drosophila
091hs1	foot -and-mo
09dsb0	foot -and-mo
091h65	foot -and-mo
091h50	foot -and-mo

105	30	71.4	98	2	05C1V3	MAGGR	051x9	magnaporthe	179	30	71.4	948	2	05O1P7	ENTH	03315	arabidopsis
106	30	71.4	129	2	06C3V3	TLUTA	06cwb3	kluyveriomyc	180	30	71.4	1029	2	05O315	ARATH	03315	arabidopsis
107	30	71.4	145	1	R1L1	COXBU	083et4	coxiella bu	181	30	71.4	1132	2	04B992	USTMA	03315	arabidopsis
108	30	71.4	151	2	09F2U2	GVIRU	09fuz2	pseudomonas	182	30	71.4	1212	2	051T95	YAGRA	051e95	mannaporthe
109	30	71.4	152	2	06HEH7	BACBK	06eh7	bacillus th	183	30	71.4	1284	2	06CDM2	YAKU	06cm2	xarowita 1i
110	30	71.4	162	2	0819U0	BACCR	081910	bacillus ce	184	30	71.4	1333	2	05SC41	DICDI	05sc41	dicyostelei
111	30	71.4	162	2	081MP4	BACAN	081mp4	bacillus an	185	30	71.4	1365	2	06FP90	ACTUM	06fp90	actinobact
112	30	71.4	162	2	0635U0	BACAZ	0635u0	bacillus ill	186	30	71.4	1365	2	05A214	BRNNU	05a214	brachyact
113	30	71.4	171	2	0888S7	LACPL	0888s7	lactococcus	187	30	71.4	1372	2	04F0H3	CHNNU	04f0h3	chrysothec
114	30	71.4	172	2	04YT75	PLABE	04yt75	plasmodium	188	30	71.4	1448	2	0612X2	SOLDE	0612x2	solanum dem
115	30	71.4	196	1	RCG1	MOUSE	03125	mus musculus	189	30	71.4	1758	2	0543E6	DIYDI	0543e6	dicyostelei
116	30	71.4	198	2	0838B7	ENTFA	0838b7	entamoeba	190	30	71.4	1918	2	04O4X2	LEITMA	04o4x2	leishmania
117	30	71.4	200	2	084U93	ARATH	084uj3	arabidopsis	191	30	71.4	1994	2	04O4X2	LEITMA	04o4x2	leishmania
118	30	71.4	200	2	084U93	ARATH	084uj3	arabidopsis	192	30	71.4	2077	2	06R9X3	NEUCR	06r9x3	neurospora
119	30	71.4	200	2	084U93	ARATH	084uj3	arabidopsis	193	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
120	30	71.4	200	2	084U93	ARATH	084uj3	arabidopsis	194	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
121	30	71.4	213	2	084U93	ARATH	084uj3	arabidopsis	195	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
122	30	71.4	213	2	084U93	ARATH	084uj3	arabidopsis	196	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
123	30	71.4	215	2	06H7U9	MEYAC	06h7u9	mycetozoa	197	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
124	30	71.4	215	2	06H7U9	MEYAC	06h7u9	mycetozoa	198	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
125	30	71.4	223	1	0731X7	BACCI	0731x7	bacillus ce	199	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
126	30	71.4	224	1	TRUB	METCA	06c041	methylococc	200	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
127	30	71.4	231	2	06C041	YAKU1	06c041	yarrowia 1i	201	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
128	30	71.4	231	2	05Y1G6	BRARE	05y1g6	brachydanio	202	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
129	30	71.4	252	2	091UK9	ARATH	09119	arabidopsis	203	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
130	30	71.4	270	2	095Y72	CABEL	095y72	caenorhabdi	204	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
131	30	71.4	298	2	07ZG67	THEIS	07zgr7	themsus the	205	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
132	30	71.4	298	2	07ZG67	THEIS	07zgr7	themsus the	206	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
133	30	71.4	305	2	04X825	BARCT	04xlf5	plasmodium	207	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
134	30	71.4	307	2	02X825	BARCT	02x825	archaeoglob	208	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
135	30	71.4	312	2	02X825	BARCT	02x825	archaeoglob	209	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
136	30	71.4	316	2	02X825	BARCT	02x825	archaeoglob	210	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
137	30	71.4	321	2	02X825	BARCT	02x825	archaeoglob	211	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
138	30	71.4	325	2	02X825	BARCT	02x825	archaeoglob	212	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
139	30	71.4	329	2	02X825	BARCT	02x825	archaeoglob	213	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
140	30	71.4	332	2	02X825	BARCT	02x825	archaeoglob	214	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
141	30	71.4	337	2	02X825	BARCT	02x825	archaeoglob	215	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
142	30	71.4	341	2	02X825	BARCT	02x825	archaeoglob	216	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
143	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	217	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
144	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	218	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
145	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	219	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
146	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	220	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
147	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	221	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
148	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	222	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
149	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	223	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
150	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	224	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
151	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	225	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
152	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	226	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
153	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	227	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
154	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	228	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
155	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	229	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
156	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	230	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
157	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	231	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
158	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	232	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
159	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	233	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
160	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	234	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
161	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	235	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
162	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	236	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
163	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	237	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
164	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	238	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
165	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	239	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
166	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	240	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
167	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	241	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
168	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	242	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
169	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	243	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
170	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	244	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
171	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	245	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
172	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	246	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
173	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	247	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
174	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	248	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
175	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	249	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
176	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	250	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
177	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	251	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
178	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	252	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
179	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	253	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
180	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	254	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
181	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	255	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
182	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	256	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora
183	30	71.4	343	2	02X825	BARCT	02x825	archaeoglob	257	30	71.4	2882	2	06R9X3	NEUCR	06r9x3	neurospora

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:21 ; Search time 17.449 Seconds
(without alignments)
42.643 Million cell updates/sec

Title: US-10-067-484-2
Perfect score: 42
Sequence: 1 PTSPXATK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep:*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep:*
3: /cgn2_6/prodata/1/iaa/H COMB.pep:*
4: /cgn2_6/prodata/1/iaa/PC/US COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PC COMB.pep:*
6: /cgn2_6/prodata/1/iaa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	76.2	232	2	US-09-489-039A-7297
2	30	71.4	100	2	US-09-198-452A-502
3	30	71.4	154	2	US-09-489-039A-15010
4	30	71.4	214	2	US-09-134-000C-4529
5	30	71.4	287	2	US-09-252-991A-23091
6	30	71.4	441	2	US-09-328-352-6369
7	30	71.4	987	2	US-09-540-236-3017
8	30	71.4	1380	2	US-09-328-352-8132
9	30	71.4	2626	2	US-09-477-962-106
10	29	69.0	92	2	US-09-248-796A-17403
11	29	69.0	106	1	US-08-800-198-4
12	29	69.0	106	2	US-09-296-595-4
13	29	69.0	231	2	US-09-248-796A-15529
14	29	69.0	239	1	US-07-956-399-4
15	29	69.0	240	1	US-08-800-198-8
16	29	69.0	240	2	US-09-296-595-8
17	29	69.0	232	2	US-09-328-352-6267
18	29	69.0	302	2	US-09-248-796A-14926
19	29	69.0	340	1	US-09-134-001C-5182
20	29	69.0	466	1	US-08-432-016-4
21	29	69.0	466	1	US-08-684-594-4
22	29	69.0	756	2	US-09-248-796A-19709
23	29	69.0	785	2	US-09-902-540-10007
24	29	69.0	935	2	US-09-134-000C-6493
25	29	69.0	1514	1	US-08-853-310-4
26	28	66.7	34	2	US-09-100-600A-6
27	28	66.7	34	2	US-09-100-600A-7

28	28	66.7	34	2	US-09-100-600A-12	Sequence 12, Appl
29	28	66.7	34	2	US-09-100-600A-13	Sequence 13, Appl
30	28	66.7	34	2	US-09-100-600A-20	Sequence 20, Appl
31	28	66.7	34	2	US-09-100-600A-21	Sequence 21, Appl
32	28	66.7	36	2	US-09-100-600A-4	Sequence 4, Appl
33	28	66.7	36	2	US-09-100-600A-5	Sequence 5, Appl
34	28	66.7	36	2	US-09-100-600A-10	Sequence 10, Appl
35	28	66.7	36	2	US-09-100-600A-11	Sequence 11, Appl
36	28	66.7	45	2	US-09-100-600A-87	Sequence 87, Appl
37	28	66.7	45	2	US-09-100-600A-88	Sequence 88, Appl
38	28	66.7	45	2	US-09-100-600A-89	Sequence 89, Appl
39	28	66.7	45	2	US-09-100-600A-90	Sequence 90, Appl
40	28	66.7	45	2	US-09-100-600A-91	Sequence 91, Appl
41	28	66.7	46	2	US-09-100-600A-41	Sequence 41, Appl
42	28	66.7	46	2	US-09-270-767-37739	Sequence 37739, A
43	28	66.7	46	2	US-09-270-767-52956	Sequence 52956, A
44	28	66.7	47	2	US-09-100-600A-67	Sequence 67, Appl
45	28	66.7	47	2	US-09-100-600A-68	Sequence 68, Appl
46	28	66.7	47	2	US-09-100-600A-70	Sequence 70, Appl
47	28	66.7	47	2	US-09-100-600A-71	Sequence 71, Appl
48	28	66.7	47	2	US-09-100-600A-72	Sequence 72, Appl
49	28	66.7	47	2	US-09-100-600A-73	Sequence 73, Appl
50	28	66.7	47	2	US-09-100-600A-74	Sequence 74, Appl
51	28	66.7	47	2	US-09-100-600A-75	Sequence 75, Appl
52	28	66.7	47	2	US-09-100-600A-76	Sequence 76, Appl
53	28	66.7	47	2	US-09-100-600A-77	Sequence 77, Appl
54	28	66.7	47	2	US-09-100-600A-78	Sequence 78, Appl
55	28	66.7	47	2	US-09-100-600A-80	Sequence 80, Appl
56	28	66.7	47	2	US-09-100-600A-81	Sequence 81, Appl
57	28	66.7	47	2	US-09-100-600A-82	Sequence 82, Appl
58	28	66.7	47	2	US-09-100-600A-83	Sequence 83, Appl
59	28	66.7	47	2	US-09-100-600A-84	Sequence 84, Appl
60	28	66.7	47	2	US-09-100-600A-85	Sequence 85, Appl
61	28	66.7	47	2	US-09-100-600A-86	Sequence 86, Appl
62	28	66.7	56	2	US-09-100-414B-103	Sequence 103, Appl
63	28	66.7	56	2	US-09-100-600A-31	Sequence 31, Appl
64	28	66.7	56	2	US-09-303-323-103	Sequence 103, Appl
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SUMMARIES

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9	32	76.2	148	US-10-767-701-48958
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90	29	69.0	1060	US-11-097-143-21204	Sequence 21204, App
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98	28	66.7	61	US-10-425-115-321847	Sequence 321847, App
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:04 ; Search time 7.89796 Seconds
(without alignments)
48.418 Million cell updates/sec

Title: US-10-067-484-2
Perfect score: 42
Sequence: 1 PTFXMARK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA New:*
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2: /SIDSS/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
3: /SIDSS/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	78.6	605	US-11-087-099-3240	Sequence 3240, App
2	32	76.2	467	US-11-079-463-8954	Sequence 8954, App
3	32	76.2	713	US-11-052-554A-74	Sequence 74, Appl
4	31	73.8	1380	US-11-079-463-6036	Sequence 6036, App
5	30	71.4	426	US-10-467-657-2120	Sequence 2120, App
6	30	71.4	899	US-11-188-298-20608	Sequence 20608, A
7	29	69.0	107	US-11-004-590-234	Sequence 234, App
8	29	69.0	107	US-11-004-590-236	Sequence 236, App
9	29	69.0	107	US-11-004-590-275	Sequence 275, App
10	29	69.0	107	US-11-004-590-276	Sequence 276, App
11	29	69.0	107	US-11-004-590-277	Sequence 277, App
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109	28	66.7	109	6	US-11-127-677-69	Sequence 69, App	182	27	64.3	747	7	US-11-113-424-26	Sequence 26, App
110	28	66.7	111	7	US-11-208-432-53	Sequence 53, App	183	27	64.3	792	7	US-10-878-688-123	Sequence 126, App
111	28	66.7	111	7	US-11-208-432-19	Sequence 19, App	184	27	64.3	886	6	US-11-098-298-9633	Sequence 9833, App
112	28	66.7	121	7	US-11-096-568A-8366	Sequence 8366, App	185	27	64.3	918	7	US-11-188-298-10721	Sequence 10721, App
113	28	66.7	121	7	US-11-188-298-12258	Sequence 12258, App	186	27	64.3	968	7	US-11-098-668-19721	Sequence 10883, App
114	28	66.7	228	7	US-11-096-568A-8365	Sequence 8365, App	187	27	64.3	1083	7	US-11-188-298-10883	Sequence 2, App
115	28	66.7	274	6	US-10-878-556A-24	Sequence 24, App	188	27	64.3	1163	7	US-11-044-899-12	Sequence 3, App
116	28	66.7	289	7	US-11-096-568A-9987	Sequence 9987, App	189	27	64.3	1363	7	US-11-052-554A-172	Sequence 172, App
117	28	66.7	314	7	US-11-079-463-6851	Sequence 6851, App	190	27	64.3	1543	7	US-11-188-298-87788	Sequence 3665, App
118	28	66.7	314	7	US-11-079-463-7384	Sequence 7384, App	191	27	64.3	1837	7	US-11-188-298-3665	Sequence 21700, App
119	28	66.7	341	7	US-11-096-568A-9986	Sequence 9986, App	192	27	64.3	1957	7	US-11-188-298-21700	Sequence 6660, App
120	28	66.7	344	7	US-11-096-568A-6580	Sequence 6580, App	193	27	64.3	2067	7	US-11-079-463-6660	Sequence 15233, App
121	28	66.7	346	7	US-11-087-039-6518	Sequence 6518, App	194	27	64.3	218	7	US-11-188-298-15233	Sequence 7760, App
122	28	66.7	349	7	US-11-087-039-1693	Sequence 1693, App	195	27	64.3	237	7	US-11-096-568A-17760	Sequence 4255, App
123	28	66.7	349	7	US-11-087-039-1693	Sequence 1693, App	196	27	64.3	240	7	US-11-096-568A-95087	Sequence 29311, App
124	28	66.7	377	7	US-11-079-463-8591	Sequence 8591, App	197	27	64.3	263	6	US-10-714-887-246	Sequence 246, App
125	28	66.7	364	7	US-11-000-453-8024	Sequence 8591, App	198	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
126	28	66.7	364	7	US-11-000-453-802	Sequence 805, App	199	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
127	28	66.7	384	7	US-11-000-453-806	Sequence 807, App	200	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
128	28	66.7	384	7	US-11-000-453-806	Sequence 807, App	201	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
129	28	66.7	384	7	US-11-000-453-807	Sequence 9875, App	202	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
130	28	66.7	428	6	US-11-096-568A-9985	Sequence 9885, App	203	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
131	28	66.7	430	7	US-11-126-313-35	Sequence 35, App	204	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
132	28	66.7	430	7	US-11-126-313-35	Sequence 35, App	205	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
133	28	66.7	593	7	US-11-169-041-839	Sequence 2497, App	206	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
134	28	66.7	619	7	US-11-072-512-4497	Sequence 2497, App	207	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
135	28	66.7	682	7	US-11-079-463-5721	Sequence 5721, App	208	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
136	28	66.7	725	6	US-10-499-290-3	Sequence 3, App	209	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
137	28	66.7	923	7	US-11-007-428-6	Sequence 6, App	210	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
138	28	66.7	1075	7	US-11-089-551A-23	Sequence 23, App	211	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
139	27	64.3	160	7	US-11-079-463-7473	Sequence 7473, App	212	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
140	27	64.3	178	7	US-11-096-568A-3521	Sequence 3521, App	213	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
141	27	64.3	219	7	US-11-205-883A-2	Sequence 2, App	214	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
142	27	64.3	223	7	US-11-079-463-6075	Sequence 6075, App	215	27	64.3	263	7	US-11-087-039-3616	Sequence 3616, App
143	27	64.3	229	6	US-10-063-707-148	Sequence 48, App	216	27	64.3	301	7	US-11-188-298-360	Sequence 360, App
144	27	64.3	229	6	US-10-194-487-198	Sequence 198, App	217	27	64.3	307	7	US-11-188-298-5760	Sequence 5760, App
145	27	64.3	229	6	US-10-195-883-198	Sequence 198, App	218	27	64.3	308	7	US-11-096-568A-29339	Sequence 29339, App
146	27	64.3	229	6	US-10-195-888-198	Sequence 198, App	219	27	64.3	310	7	US-11-188-298-12746	Sequence 12746, App
147	27	64.3	229	6	US-10-195-888-198	Sequence 198, App	220	27	64.3	310	7	US-11-096-568A-4487	Sequence 4487, App
148	27	64.3	229	6	US-11-102-240-48	Sequence 48, App	221	27	64.3	311	7	US-11-096-568A-4485	Sequence 4485, App
149	27	64.3	229	6	US-11-103-195-48	Sequence 48, App	222	27	64.3	312	7	US-11-096-568A-4485	Sequence 4485, App
150	27	64.3	289	7	US-11-188-298-3378	Sequence 3378, App	223	27	64.3	322	7	US-11-188-298-10108	Sequence 10108, App
151	27	64.3	303	7	US-11-079-463-8594	Sequence 8594, App	224	27	64.3	322	7	US-11-188-298-12208	Sequence 12208, App
152	27	64.3	347	7	US-11-096-568A-32503	Sequence 32503, App	225	27	64.3	324	7	US-11-188-298-1364	Sequence 1364, App
153	27	64.3	376	7	US-11-096-568A-19994	Sequence 19994, App	226	27	64.3	324	7	US-11-096-568A-21907	Sequence 21907, App
154	27	64.3	406	7	US-11-096-568A-19992	Sequence 19992, App	227	27	64.3	324	7	US-11-188-298-824	Sequence 824, App
155	27	64.3	406	7	US-11-113-424-72	Sequence 72, App	228	27	64.3	324	7	US-11-188-298-6472	Sequence 6472, App
156	27	64.3	450	7	US-11-096-568A-31401	Sequence 31401, App	229	27	64.3	324	7	US-11-188-298-18570	Sequence 18570, App
157	27	64.3	450	7	US-11-096-568A-31401	Sequence 31401, App	230	27	64.3	324	7	US-11-188-298-18570	Sequence 18570, App
158	27	64.3	470	7	US-11-087-039-9531	Sequence 31400, App	231	27	64.3	331	7	US-11-188-298-12215	Sequence 12215, App
159	27	64.3	481	7	US-11-096-568A-33459	Sequence 33459, App	232	27	64.3	333	7	US-11-188-298-12215	Sequence 12215, App
160	27	64.3	503	7	US-11-113-424-72	Sequence 72, App	233	27	64.3	344	7	US-11-096-568A-32172	Sequence 32172, App
161	27	64.3	519	7	US-11-087-039-6772	Sequence 6772, App	234	27	64.3	344	7	US-11-188-298-6045	Sequence 6045, App
162	27	64.3	519	7	US-11-188-298-17207	Sequence 17207, App	235	27	64.3	344	7	US-11-096-568A-21906	Sequence 21906, App
163	27	64.3	532	7	US-11-096-568A-31399	Sequence 31399, App	236	27	64.3	359	7	US-11-087-039-5586	Sequence 5586, App
164	27	64.3	532	7	US-11-188-298-30660	Sequence 20660, App	237	27	64.3	359	7	US-11-087-039-5586	Sequence 5586, App
165	27	64.3	532	7	US-11-188-298-30660	Sequence 20660, App	238	27	64.3	359	7	US-11-087-039-5586	Sequence 5586, App
166	27	64.3	536	7	US-11-188-298-20728	Sequence 1793, App	239	27	64.3	360	7	US-11-188-298-3577	Sequence 7664, App
167	27	64.3	553	7	US-11-087-039-1793	Sequence 1793, App	240	27	64.3	415	7	US-11-188-298-7864	Sequence 7864, App
168	27	64.3	555	7	US-11-087-039-5222	Sequence 5222, App	241	27	64.3	447	7	US-11-087-039-979	Sequence 979, App
169	27	64.3	555	7	US-11-096-568A-33458	Sequence 33458, App	242	27	64.3	448	7	US-11-188-298-15913	Sequence 15913, App
170	27	64.3	560	7	US-11-096-568A-33457	Sequence 33457, App	243	27	64.3	455	7	US-11-188-298-21716	Sequence 21716, App
171	27	64.3	570	7	US-11-113-424-69	Sequence 69, App	244	27	64.3	468	7	US-11-188-298-9902	Sequence 9902, App

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:40:47 ; Search time 90.7347 Seconds

(without alignments)
43.582 Million cell updates/sec

Title: US-10-067-484-3

Perfect score: 43

Sequence: 1 XYGLVQFNR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_21:*

1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20016:*
5: geneseqp20025:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	9	5	ABB81970 Abb81970 30 kDa ra
2	33	76.7	99	4	AAU56543 Aau56543 Propionib
3	33	76.7	99	4	ABM53062 Abm53062 Propionib
4	33	76.7	170	6	ABU28434 Abu28434 Protein e
5	33	76.7	192	7	ADM26790 Adm26790 Hyperther
6	33	76.7	253	5	ABP25912 Abp25912 Streptococ
7	33	76.7	253	8	ADV88395 Adv88395 Streptococ
8	33	76.7	253	8	ADV81810 Adv81810 Streptococ
9	33	76.7	253	8	ADV79648 Adv79648 Streptococ
10	33	76.7	329	3	AAU51794 Aau51794 Gene 21 h
11	33	76.7	329	3	AAU51794 Aau51794 Gene 21 h
12	33	76.7	383	9	AEA28843 Aea28843 Pseudomon
13	33	76.7	819	9	ADA33363 Ada33363 Acinetoba
14	33	76.7	16	9	ADY38298 Ady38298 Human CYP
15	33	76.7	16	9	ADY38298 Ady38298 Human CYP
16	33	76.7	16	9	ADY38298 Ady38298 Human CYP
17	33	76.7	16	9	ADY38298 Ady38298 Human CYP
18	33	76.7	16	9	ADY38298 Ady38298 Human CYP
19	33	76.7	16	9	ADY38298 Ady38298 Human CYP
20	33	76.7	16	9	ADY38298 Ady38298 Human CYP
21	33	76.7	16	9	ADY38298 Ady38298 Human CYP
22	33	76.7	16	9	ADY38298 Ady38298 Human CYP
23	33	76.7	16	9	ADY38298 Ady38298 Human CYP
24	33	76.7	16	9	ADY38298 Ady38298 Human CYP

25	32	74.4	124	8	ADP19441 Adp19441 Human sec
26	32	74.4	124	8	ADP19471 Adp19471 Human sec
27	32	74.4	132	2	AAV76521 Aav76521 Human ova
28	32	74.4	132	2	AAV76521 Aav76521 Human ova
29	32	74.4	291	5	ABG91467 Abg91467 Human pol
30	32	74.4	291	5	ABG91467 Abg91467 Human pol
31	32	74.4	291	5	ABG91467 Abg91467 Human pol
32	32	74.4	291	5	ABG91467 Abg91467 Human pol
33	32	74.4	291	5	ABG91467 Abg91467 Human pol
34	32	74.4	291	5	ABG91467 Abg91467 Human pol
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98	30	69.8	652	9	ADY60941	Ady60941	Abiotic B	171	29	67.4	292	5	ABG91423	Abg91423	Purine/py
99	30	69.8	712	8	ADN47190	Adn47190	Thermococ	172	29	67.4	293	5	ABG91428	Abg91428	Purine/py
100	30	69.8	712	8	ADN29538	Adn29538	Protein e	173	29	67.4	293	5	ABG91429	Abg91429	Purine/py
101	30	69.8	748	2	AAW13384	Aaw13384	Human pro	174	29	67.4	293	8	ADN18234	Adn18234	Bacterial
102	30	69.8	748	2	ADN31277	Adn31277	Human aci	175	29	67.4	293	8	ABM83480	Abm83480	Human dia
103	30	69.8	748	2	ADN95750	Adn95750	Human BRC	176	29	67.4	296	2	AAE55350	Aae55350	Wheat lea
104	30	69.8	748	2	ADN32103	Adn32103	Human tnm	177	29	67.4	303	5	ADG79547	Adg79547	Human sec
105	30	69.8	748	2	ADY06044	Ady06044	Cyclin-de	178	29	67.4	304	3	AAE25236	Aae25236	Arabidops
106	30	69.8	748	2	ADY15588	Ady15588	PRO polyP	179	29	67.4	306	8	ADY11224	Ady11224	Plant ful
107	30	69.8	752	8	ADN27508	Adn27508	Bacterial	180	29	67.4	316	4	ABE62195	AbE62195	Drosophi
108	30	69.8	752	8	ADN35195	Adn35195	Enterococ	181	29	67.4	325	8	ADN19887	Adn19887	Bacterial
109	30	69.8	752	6	ABU29144	Abu29144	Protein e	182	29	67.4	377	8	ADN47167	Adn47167	Thermococ
110	30	69.8	752	7	ADG94066	Adg94066	E. faeciu	183	29	67.4	390	4	AAE75221	Aae75221	Drosophi
111	30	69.8	804	4	ADN19610	Adn19610	Human dia	184	29	67.4	390	5	AAE30519	Aae30519	Fruit fly
112	30	69.8	831	8	ADN05464	Adn05464	Antipepti	185	29	67.4	390	6	ABU29664	Abu29664	Protein e
113	30	69.8	932	6	ADN05464	Adn05464	Protein e	186	29	67.4	395	4	ABE66004	AbE66004	Drosophi
114	30	69.8	960	6	ABP97913	Abp97913	Amnio aci	187	29	67.4	414	8	ADY23962	Ady23962	Plant ful
115	30	69.8	1035	4	ABE61120	AbE61120	Drosophi	188	29	67.4	419	3	AAE53327	Aae53327	Arabidops
116	30	69.8	1038	6	ABU25711	Abu25711	Protein e	189	29	67.4	437	4	ABG17017	Abg17017	Novel hum
117	30	69.8	1179	6	ABU27677	Abu27677	Listeria	190	29	67.4	460	6	ABE63425	AbE63425	Drosophi
118	30	69.8	1179	6	ABU32719	Abu32719	Protein e	191	29	67.4	466	6	ABE53249	AbE53249	Protein s
119	30	69.8	1874	4	AAE76532	Aae76532	Corynebac	192	29	67.4	476	7	ADK63662	Adk63662	Disease t
120	30	69.8	2071	5	ABE74125	AbE74125	Mouse mas	193	29	67.4	482	7	ADG08285	Adg08285	Rice prot
121	30	69.8	2701	5	ABE74125	AbE74125	Human TRI	194	29	67.4	487	6	ABU49180	Abu49180	Protein e
122	30	69.8	2747	8	ADN62964	Adn62964	Human NOV	195	29	67.4	480	3	AAE53682	Aae53682	Arabidops
123	30	69.8	2753	6	ADN62964	Adn62964	Human NOV	196	29	67.4	480	3	AAE07398	Aae07398	Arabidops
124	30	69.8	2753	6	ADN62964	Adn62964	Human NOV	197	29	67.4	485	3	AAE53681	Aae53681	Arabidops
125	30	69.8	2753	6	ADN62964	Adn62964	Human NOV	198	29	67.4	485	3	AAE53681	Aae53681	Arabidops
126	30	69.8	2777	8	AAE10925	Aae10925	Human mon	199	29	67.4	487	8	ADK23232	Adk23232	Wheat lea
127	30	69.8	2777	8	ADU47185	Adu47185	Human mon	200	29	67.4	500	2	AAE83351	Aae83351	Protein
128	30	69.8	2780	4	AAE10924	Aae10924	Mouse mon	201	29	67.4	500	5	ABE48229	AbE48229	Arabidops
129	30	69.8	2969	7	ADL65607	Adl65607	C. glutam	202	29	67.4	500	9	ABE48229	AbE48229	Arabidops
130	30	69.8	2969	7	ADL65607	Adl65607	C. glutam	203	29	67.4	503	3	ABE48229	AbE48229	Arabidops
131	30	69.8	3040	8	ADN88306	Adn88306	Brevibact	204	29	67.4	514	5	ABG91767	Abg91767	Purine/py
132	30	69.8	3040	8	ADN88306	Adn88306	Brevibact	205	29	67.4	514	5	ABG91767	Abg91767	Purine/py
133	30	69.8	3062	8	ADQ26411	Adq26411	Brevibact	206	29	67.4	517	3	AAE46463	Aae46463	Arabidops
134	30	69.8	3062	8	ADQ26411	Adq26411	Brevibact	207	29	67.4	517	3	AAE46463	Aae46463	Arabidops
135	30	69.8	3062	8	ADQ26411	Adq26411	Brevibact	208	29	67.4	518	9	ABE48227	AbE48227	Arabidops
136	30	69.8	3338	6	ADN05802	Adn05802	Human NOV	209	29	67.4	519	2	AAE11526	Aae11526	Rice ADP-
137	30	69.8	3338	6	ADN05802	Adn05802	Human NOV	210	29	67.4	519	5	ABG91127	Abg91127	Rice ADP-
138	30	69.8	6298	8	ADN05802	Adn05802	Human NOV	211	29	67.4	519	5	ABG91127	Abg91127	Rice ADP-
139	30	69.8	6298	8	ADN05802	Adn05802	Human NOV	212	29	67.4	521	7	ABG91128	Abg91128	Rice prot
140	30	69.8	6306	8	ADN05802	Adn05802	Human NOV	213	29	67.4	522	5	AAE31865	Aae31865	Arabidops
141	30	69.8	6306	8	ADN05802	Adn05802	Human NOV	214	29	67.4	522	5	AAE31865	Aae31865	Arabidops
142	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	215	29	67.4	522	7	ADK28898	Adk28898	Tall fesc
143	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	216	29	67.4	522	7	ADK28898	Adk28898	Tall fesc
144	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	217	29	67.4	523	5	ABG91731	Abg91731	Purine/py
145	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	218	29	67.4	523	5	ABG91731	Abg91731	Purine/py
146	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	219	29	67.4	527	2	AAE63446	Aae63446	Arabidops
147	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	220	29	67.4	527	5	ABG91733	Abg91733	Purine/py
148	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	221	29	67.4	529	5	ABG91733	Abg91733	Purine/py
149	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	222	29	67.4	530	8	ADY76093	Ady76093	Plant ful
150	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	223	29	67.4	531	7	ADG07870	Adg07870	Rice prot
151	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	224	29	67.4	533	8	ADY74311	Ady74311	Plant ful
152	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	225	29	67.4	533	8	ADY74311	Ady74311	Plant ful
153	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	226	29	67.4	540	7	ADG07874	Adg07874	Rice prot
154	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	227	29	67.4	547	3	AAE46482	Aae46482	Arabidops
155	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	228	29	67.4	547	3	AAE46482	Aae46482	Arabidops
156	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	229	29	67.4	559	3	AAE46481	Aae46481	Arabidops
157	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	230	29	67.4	559	6	ABU01457	Abu01457	Iron upla
158	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	231	29	67.4	559	6	ABU01457	Abu01457	Iron upla
159	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	232	29	67.4	559	8	ADK47220	Adk47220	Streptoco
160	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	233	29	67.4	559	8	ADK47220	Adk47220	Streptoco
161	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	234	29	67.4	562	3	AAE33680	Aae33680	Arabidops
162	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	235	29	67.4	562	3	AAE33680	Aae33680	Arabidops
163	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	236	29	67.4	562	3	AAE33680	Aae33680	Arabidops
164	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	237	29	67.4	562	3	AAE33680	Aae33680	Arabidops
165	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	238	29	67.4	562	3	AAE33680	Aae33680	Arabidops
166	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	239	29	67.4	562	3	AAE33680	Aae33680	Arabidops
167	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	240	29	67.4	562	3	AAE33680	Aae33680	Arabidops
168	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	241	29	67.4	562	3	AAE33680	Aae33680	Arabidops
169	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	242	29	67.4	562	3	AAE33680	Aae33680	Arabidops
170	30	69.8	6307	9	ADN05802	Adn05802	Human NOV	243	29	67.4	562	3	AAE33680	Aae33680	Arabidops

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:12 ; Search time 8.26511 Seconds
(without alignments)
104.769 Million cell updates/sec

Title: US-10-067-484-3
Perfect score: 43
Sequence: 1 XYGIVQFNR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: PIR 80: *
2: PIR1: *
3: PIR2: *
4: PIR3: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	76.7	63	2 D69115	hypothetical prote
2	33	76.7	650	2 T32897	hypothetical prote
3	33	76.7	662	2 T47649	ABC transporter-li
4	32	74.4	296	2 H90896	hypothetical prote
5	32	74.4	296	2 G85720	hypothetical prote
6	32	74.4	296	2 B64908	yeah protein - Bsc
7	32	74.4	417	2 C69795	glutanyl-tRNA (Gln)
8	32	74.4	476	2 T51583	glutanyl-tRNA (Gln)
9	32	74.4	476	2 T44293	glutanyl-tRNA (Gln)
10	32	74.4	751	2 D71860	probable outer mem
11	31	72.1	152	2 B64842	probable monooxyge
12	31	72.1	152	2 B90785	probable 4-hydroxy
13	31	72.1	152	2 C85645	probable 4-hydroxy
14	31	72.1	345	2 A70474	N-acetyl-gamma-glu
15	31	72.1	364	2 A70474	conserved hypotet
16	31	72.1	428	2 T03934	DNA binding protei
17	31	72.1	482	2 T01932	RNA binding protei
18	31	72.1	570	2 C86440	PPR-repeat protei
19	31	72.1	791	2 S61658	hypothetical prote
20	31	72.1	794	1 S37606	SRG18 protein - ye
21	31	72.1	3655	2 T38084	TRAP-like protein
22	30	69.8	47	2 F81235	hypothetical prote
23	30	69.8	81	2 T06548	RNA-directed DNA p
24	30	69.8	88	2 B47760	retrovirus-related
25	30	69.8	123	2 T43380	ribosomal protein
26	30	69.8	133	2 G91092	hypothetical prote
27	30	69.8	136	2 T19479	60s ribosomal prot
28	30	69.8	136	2 T19479	hypothetical prote
29	30	69.8	167	2 C85938	hypothetical prote

30	30	69.8	207	2 T03331	gene e36 protein -
31	30	69.8	223	2 H87335	conserved hypotet
32	30	69.8	229	2 A81169	hypothetical prote
33	30	69.8	231	2 G81936	hypothetical prote
34	30	69.8	282	2 A97512	glucose 1-dehydrog
35	30	69.8	286	2 D75597	glucose-1-phosphat
36	30	69.8	297	2 AC1706	hypothetical prote
37	30	69.8	297	2 AD1335	hypothetical prote
38	30	69.8	304	2 S24263	seed storage prote
39	30	69.8	357	2 G86906	hypothetical prote
40	30	69.8	400	2 G83790	aminotransferase B
41	30	69.8	404	2 F71718	alanine racemase (
42	30	69.8	408	2 C70379	hypothetical prote
43	30	69.8	449	2 T48511	aspartate transami
44	30	69.8	468	2 T33516	hypothetical prote
45	30	69.8	474	2 AB2161	hypothetical prote
46	30	69.8	514	2 B84290	hypothetical prote
47	30	69.8	548	2 T41182	probable protein p
48	30	69.8	555	2 A45697	immediate-early pr
49	30	69.8	584	2 G82079	single-stranded-DN
50	30	69.8	638	2 S37085	polyadenylate-bind
51	30	69.8	651	2 T06979	polyadenylate-bind
52	30	69.8	655	2 T00768	polyadenylate-bind
53	30	69.8	668	2 B96740	hypothetical prote
54	30	69.8	720	2 A13420	hypothetical prote
55	30	69.8	720	2 T47648	ABC transporter-li
56	30	69.8	757	2 AC2691	penicillin binding
57	30	69.8	757	2 G97472	penicillin-binding
58	30	69.8	867	1 RRVGCV	RNA-directed RNA p
59	30	69.8	967	2 T15680	hypothetical prote
60	30	69.8	1179	2 AG1101	transcription-repa
61	30	69.8	1179	2 AG1463	transcription-repa
62	30	69.8	1179	2 S55505	fatty-acid synchas
63	30	69.8	285	2 AG2963	conserved hypotet
64	29.5	68.6	320	2 F98319	hypothetical prote
65	29	67.4	93	2 A72653	hypothetical prote
66	29	67.4	149	2 S22209	photosystem I chla
67	29	67.4	168	2 H89886	hypothetical prote
68	29	67.4	220	1 YVBPFE	phage lysis protei
69	29	67.4	227	2 C58932	channel subunit of
70	29	67.4	229	2 A37775	phob protein - Pse
71	29	67.4	229	2 AG0698	probable pathogeni
72	29	67.4	232	2 T44456	arginine/oritidine
73	29	67.4	277	2 H70159	ribosomal protein
74	29	67.4	288	2 AE1313	hypothetical prote
75	29	67.4	288	2 AE1585	hypothetical prote
76	29	67.4	289	2 A87391	glucose-1-phosphat
77	29	67.4	290	1 S06477	enoyl-CoA hydratase
78	29	67.4	293	1 F64969	glucose-1-phosphat
79	29	67.4	294	2 C72378	sugar ABC transport
80	29	67.4	296	2 S05078	glucose-1-phosphat
81	29	67.4	333	2 D97356	uncharacterized pr
82	29	67.4	343	2 S77079	hypothetical prote
83	29	67.4	343	2 D96900	recP, ABC family A
84	29	67.4	363	2 D66900	hypothetical prote
85	29	67.4	384	2 S64074	hypothetical prote
86	29	67.4	402	2 T25363	hypothetical prote
87	29	67.4	410	2 T15442	hypothetical prote
88	29	67.4	442	2 H69181	NADH2 dehydrogenas
89	29	67.4	462	2 T11136	PEP12 homolog - M
90	29	67.4	472	2 A64320	dolichyl-diphospho
91	29	67.4	476	2 A65610	probable glu-tRNA
92	29	67.4	486	2 B72554	D-alanyl-D-alanine
93	29	67.4	487	2 H82298	glutanyl-tRNA (Gln)
94	29	67.4	491	2 A11980	glucose-1-phosphat
95	29	67.4	500	2 S05077	hypothetical prote
96	29	67.4	502	2 G70193	hypothetical prote
97	29	67.4	514	2 T04155	glucose-1-phosphat
98	29	67.4	518	2 T02965	glucose-1-phosphat
99	29	67.4	519	2 T02965	glucose-1-phosphat
100	29	67.4	521	2 S49439	glucose-1-phosphat
101	29	67.4	522	2 S60572	glucose-1-phosphat
102	29	67.4	527	2 S24984	glucose-1-phosphat
	29	67.4	559	2 B95120	site-specific reco

103	29	67.4	559	2	F971989	site-specific recco	176	28	65.1	536	2	T049398	hypothetical prote
104	29	67.4	552	2	A967193	hypothetical prote	177	28	65.1	546	2	B85398	hypothetical prote
105	29	67.4	570	2	G88098	protein p18A12.3 l	178	28	65.1	563	2	F971028	arginyl-tRNA synth
106	29	67.4	581	1	B86810	probable transpor sy	179	28	65.1	586	2	S34383	calpain (EC 3.4.22
107	29	67.4	609	2	B84783	polyadenylate-bind	180	28	65.1	629	2	A47398	serotoninn transpor
108	29	67.4	662	2	T00497	hypothetical prote	181	28	65.1	630	1	STAMP	serine proteinase
109	29	67.4	689	2	G84447	collin-4 - fission	182	28	65.1	655	1	G86397	protein TVN9.18 (1
110	29	67.4	734	2	T43505	probable ATP-bindi	183	28	65.1	657	2	C71905	conserved hypothet
111	29	67.4	740	1	T43505	probable isoenzyme	184	28	65.1	660	2	F64608	probable outer mem
112	29	67.4	1047	2	AM1208	pyruvate carboxyla	185	28	65.1	668	2	D71879	ribonuclease E (rn
113	29	67.4	1146	2	AC1565	RNA polymerase bet	186	28	65.1	683	2	D71860	ribonuclease E (rn
114	29	67.4	1188	2	B82533	RNA polymerase bet	187	28	65.1	690	2	F97742	hyponuclease E (EC
115	29	67.4	1497	2	S47890	experimental i - fr	188	28	65.1	691	2	D90592	conserved hypothet
116	29	65.1	69	2	D90905	hypothetical prote	189	28	65.1	700	2	B54566	calpain (EC 3.4.22
117	29	65.1	69	2	D90905	transcriptional regu	190	28	65.1	705	2	C75118	protein-RNA-bindi
118	29	65.1	88	2	T42909	hypothetical prote	191	28	65.1	714	1	CIHH	protein-RNA-bindi
119	29	65.1	116	2	D97755	hypothetical prote	192	28	65.1	738	1	T38767	insulin activator
120	29	65.1	183	2	A12274	hypothetical prote	193	28	65.1	744	2	A56034	probable outer mem
121	29	65.1	185	2	AF2236	hypothetical prote	194	28	65.1	744	2	H71818	conserved hypothet
122	29	65.1	197	2	T16478	hypothetical prote	195	28	65.1	746	2	B54701	probable transmem
123	29	65.1	197	2	T16478	hypothetical prote	196	28	65.1	766	2	B75059	fatty acid cis/tra
124	29	65.1	206	2	S76189	hypothetical prote	197	28	65.1	766	2	B82445	DNA gyrase, chain B
125	29	65.1	230	2	H83001	probable enzyme C	198	28	65.1	773	2	B71931	DNA gyrase, sub B
126	29	65.1	231	2	G69387	dephosphorin oxid	199	28	65.1	773	2	B71931	outer membrane ush
127	29	65.1	252	2	H90476	hypothetical prote	200	28	65.1	835	1	B64382	probable chromet
128	29	65.1	285	2	S63260	glucose-1-phosphat	201	28	65.1	835	1	S33942	hexon protein - hu
129	29	65.1	285	2	S63260	glucose-1-phosphat	202	28	65.1	835	1	S33942	hexon protein - hu
130	29	65.1	288	2	B81240	glucose-1-phosphat	203	28	65.1	835	1	HXAD40	hexon protein - hu
131	29	65.1	288	2	B81240	glucose-1-phosphat	204	28	65.1	835	1	HXAD40	hexon protein - hu
132	29	65.1	290	2	AM1487	hypothetical prote	205	28	65.1	835	1	S57637	hexon protein - hu
133	29	65.1	290	2	AM1487	hypothetical prote	206	28	65.1	836	2	S55504	hexon protein - hu
134	29	65.1	291	2	AD0767	glucose-1-phosphat	207	28	65.1	840	2	S37216	hexon protein - hu
135	29	65.1	292	2	G23342	glucose-1-phosphat	208	28	65.1	840	2	S39298	hexon protein - hu
136	29	65.1	292	2	G23342	glucose-1-phosphat	209	28	65.1	942	1	HKXD5	hexon protein - hu
137	29	65.1	293	2	G23342	glucose-1-phosphat	210	28	65.1	952	1	HKXD5	hexon protein - hu
138	29	65.1	293	2	G23342	glucose-1-phosphat	211	28	65.1	967	1	HKXD5	hexon protein - hu
139	29	65.1	309	1	XYECM	homoserine O-succl	212	28	65.1	990	2	S67499	glutamate synthase
140	29	65.1	309	2	AC1011	homoserine O-succl	213	28	65.1	990	2	S67499	glutamate synthase
141	29	65.1	309	2	AC1011	homoserine O-succl	214	28	65.1	1071	2	F339845	reverse transcriptase
142	29	65.1	309	2	AC1011	homoserine O-succl	215	28	65.1	1146	2	B70376	reverse transcriptase
143	29	65.1	309	2	AC1011	homoserine O-succl	216	28	65.1	1212	2	F83153	reverse transcriptase
144	29	65.1	309	2	AC1011	homoserine O-succl	217	28	65.1	1267	2	T21913	reverse transcriptase
145	29	65.1	309	2	AC1011	homoserine O-succl	218	28	65.1	1474	1	MAHU	reverse transcriptase
146	29	65.1	309	2	AC1011	homoserine O-succl	219	28	65.1	1496	2	T05634	reverse transcriptase
147	29	65.1	309	2	AC1011	homoserine O-succl	220	28	65.1	1517	2	CGH034	reverse transcriptase
148	29	65.1	309	2	AC1011	homoserine O-succl	221	28	65.1	1517	2	CGH034	reverse transcriptase
149	29	65.1	309	2	AC1011	homoserine O-succl	222	28	65.1	1517	2	CGH034	reverse transcriptase
150	29	65.1	309	2	AC1011	homoserine O-succl	223	28	65.1	1517	2	CGH034	reverse transcriptase
151	29	65.1	309	2	AC1011	homoserine O-succl	224	28	65.1	1517	2	CGH034	reverse transcriptase
152	29	65.1	309	2	AC1011	homoserine O-succl	225	28	65.1	1517	2	CGH034	reverse transcriptase
153	29	65.1	309	2	AC1011	homoserine O-succl	226	28	65.1	1517	2	CGH034	reverse transcriptase
154	29	65.1	309	2	AC1011	homoserine O-succl	227	28	65.1	1517	2	CGH034	reverse transcriptase
155	29	65.1	309	2	AC1011	homoserine O-succl	228	28	65.1	1517	2	CGH034	reverse transcriptase
156	29	65.1	309	2	AC1011	homoserine O-succl	229	28	65.1	1517	2	CGH034	reverse transcriptase
157	29	65.1	309	2	AC1011	homoserine O-succl	230	28	65.1	1517	2	CGH034	reverse transcriptase
158	29	65.1	309	2	AC1011	homoserine O-succl	231	28	65.1	1517	2	CGH034	reverse transcriptase
159	29	65.1	309	2	AC1011	homoserine O-succl	232	28	65.1	1517	2	CGH034	reverse transcriptase
160	29	65.1	309	2	AC1011	homoserine O-succl	233	28	65.1	1517	2	CGH034	reverse transcriptase
161	29	65.1	309	2	AC1011	homoserine O-succl	234	28	65.1	1517	2	CGH034	reverse transcriptase
162	29	65.1	309	2	AC1011	homoserine O-succl	235	28	65.1	1517	2	CGH034	reverse transcriptase
163	29	65.1	309	2	AC1011	homoserine O-succl	236	28	65.1	1517	2	CGH034	reverse transcriptase
164	29	65.1	309	2	AC1011	homoserine O-succl	237	28	65.1	1517	2	CGH034	reverse transcriptase
165	29	65.1	309	2	AC1011	homoserine O-succl	238	28	65.1	1517	2	CGH034	reverse transcriptase
166	29	65.1	309	2	AC1011	homoserine O-succl	239	28	65.1	1517	2	CGH034	reverse transcriptase
167	29	65.1	309	2	AC1011	homoserine O-succl	240	28	65.1	1517	2	CGH034	reverse transcriptase
168	29	65.1	309	2	AC1011	homoserine O-succl	241	28	65.1	1517	2	CGH034	reverse transcriptase
169	29	65.1	309	2	AC1011	homoserine O-succl	242	28	65.1	1517	2	CGH034	reverse transcriptase
170	29	65.1	309	2	AC1011	homoserine O-succl	243	28	65.1	1517	2	CGH034	reverse transcriptase
171	29	65.1	309	2	AC1011	homoserine O-succl	244	28	65.1	1517	2	CGH034	reverse transcriptase
172	29	65.1	309	2	AC1011	homoserine O-succl	245	28	65.1	1517	2	CGH034	reverse transcriptase
173	29	65.1	309	2	AC1011	homoserine O-succl	246	28	65.1	1517	2	CGH034	reverse transcriptase
174	29	65.1	309	2	AC1011	homoserine O-succl	247	28	65.1	1517	2	CGH034	reverse transcriptase
175	29	65.1	309	2	AC1011	homoserine O-succl	248	28	65.1	1517	2	CGH034	reverse transcriptase

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:05 ; Search time 49.0408 Seconds
(without alignments)
129.479 Million cell updates/sec

Title: US-10-067-484-3
Perfect score: 43
Sequence: 1 XYGLVQFNR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	88.4	443	04MDR7 ASPFU	04wdt7 aspergillus
2	38	88.4	678	05LIH0_BACRY	05liho bacteroides
3	38	88.4	678	064ZU4_BACFR	064zf4 bacteroides
4	34	79.1	242	054P36_DICDI	054p36 dictyosteli
5	34	79.1	304	083AP7_COXBU	083ap7 coxiella bu
6	34	79.1	354	1 ARGC_BORBR	07wfc5 bordetella
7	34	79.1	354	1 ARGC_BORPA	07w323 bordetella
8	34	79.1	354	1 ARGC_BORPE	07wuo0 bordetella
9	33	76.7	63	027885_METTH	027885 methanobact
10	33	76.7	124	06Y228_PAGMA	06y228 pagrus majo
11	33	76.7	124	050386_BRARE	050386 brachydanio
12	33	76.7	124	04SSFS_TETNG	04ssfs tetradon n
13	33	76.7	192	08TVJ3_METKA	08tvj3 methanopyru
14	33	76.7	253	1 RECO_STRAS	08e7x6 streptococc
15	33	76.7	253	1 RECO_STRAS	08e298 streptococc
16	33	76.7	275	061104_CAEBR	061104 caenorhabdi
17	33	76.7	278	057UW9_STRYP	057uw9 trypanosoma
18	33	76.7	313	044967_CAEEL	044967 caenorhabdi
19	33	76.7	333	2 08SRU7_ENCCU	08sr17 encephalito
20	33	76.7	463	2 05OU64_ENTHI	05ou64 entamoeba h
21	33	76.7	533	2 08DHX4_SYNEL	08dhx4 synechococc
22	33	76.7	618	1 XYLA2_BACST	049674 bacillus st
23	33	76.7	648	2 061S93_CAEBR	061s93 caenorhabdi
24	33	76.7	662	2 09M2V6_ARATH	09m2v6 arabidopsis
25	33	76.7	1439	2 05TVAL1_ANOGA	05tval1 anopheles g
26	32	74.4	124	1 MKI11_HUMAN	09uh44 homo sapien
27	32	74.4	124	1 MKI11_MOUSE	088653 mus musculu
28	32	74.4	124	2 053F86_HUMAN	053f86 homo sapien
29	32	74.4	124	2 05R3Z6_PONPY	05r3z6 ponopygma
30	32	74.4	124	2 054217_MOUSE	054217 mus musculu
31	32	74.4	124	2 05U204_RAT	05u204 rattus norv

32	32	74.4	124	2 05Z1P2_CHICK	05z1p2 gallus gall
33	32	74.4	148	2 05K592_ORYSA	05k592 oryza sativ
34	32	74.4	166	2 05HMM0_STABO	05hmm0 staphylococ
35	32	74.4	260	2 05KUB0_GEOKA	05kub0 geobacillus
36	32	74.4	262	2 060A70_MERCA	060a70 methylococc
37	32	74.4	291	2 09RDY3_LEGEN	09rdy3 legionella
38	32	74.4	291	2 04US24_CORR	04us24 corynebact
39	32	74.4	291	2 05WYD9_LEGPH	05wyd9 legionella
40	32	74.4	291	2 05X6V7_LEGON	05x6v7 legionella
41	32	74.4	293	2 082WJ7_NITPU	082wj7 nitrosomona
42	32	74.4	296	1 YDER_ECOLI	08x26 escherichia
43	32	74.4	296	2 08XB26_ECO57	08xb26 escherichia
44	32	74.4	298	2 08FHD4_ECOL6	08fhd4 escherichia
45	32	74.4	299	2 07MGN4_WOLES	07mgn4 wolfinella s
46	32	74.4	305	2 05ZXH1_LEGPH	05zxh1 legionella
47	32	74.4	321	2 06ASCI_DESPS	06asci desulfatole
48	32	74.4	359	2 05LO45_SILPO	05lq45 silicibacte
49	32	74.4	395	2 05ZRY3_LEGPH	05zry3 legionella
50	32	74.4	399	2 07PUT5_ANOGA	07put5 anopheles g
51	32	74.4	426	2 09LIY4_ORYSA	09liy4 oryza sativ
52	32	74.4	444	2 06Z9W0_ORYSA	06z9w0 oryza sativ
53	32	74.4	444	2 082B12_STRAM	082b12 streptomyce
54	32	74.4	445	2 09P8U4_ASPEU	09p8u4 aspergillus
55	32	74.4	475	2 04MM30_ASPEU	04mm30 aspergillus
56	32	74.4	476	1 GATB_BACST	0929x0 aspergillus
57	32	74.4	476	1 GATB_BACHD	0931e1 bacillus su
58	32	74.4	476	1 GATB_BACST	030509 bacillus su
59	32	74.4	476	1 0513B2_GEOKA	0513b2 geobacillus
60	32	74.4	476	2 067KJ3_SYMRH	067kj3 symbiobacte
61	32	74.4	525	2 04WB62_ASPEU	04wb62 aspergillus
62	32	74.4	527	2 04MOB4_9BURK	04mob4 burkholderi
63	32	74.4	530	2 04ADU7_PLACH	04adu7 plasmodium
64	32	74.4	692	2 07NSR3_CHRYO	07nsr3 chromobacte
65	32	74.4	717	2 098516_RHTIO	098516 rhizobium 1
66	32	74.4	733	2 0872B5_NEUR	0872b5 neurospora
67	32	74.4	733	2 054P69_DICDI	054p69 dictyosteli
68	32	74.4	751	2 09ZKD1_HELPB	09zkd1 helicobacte
69	32	74.4	761	2 089QW2_BRAJA	089qm2 bradyrhizob
70	32	74.4	812	2 07RJ31_PLAOD	07rj31 plasmodium
71	32	74.4	821	2 0709P7_ANOGA	07g9f7 anopheles g
72	32	74.4	949	2 087Z35_METKA	087z35 methanopyru
73	32	74.4	1026	2 07RSV2_PLAIO	07rsv2 plasmodium
74	32	74.4	1109	2 04UB11_THENX	04ub11 theileria a
75	32	74.4	1136	2 07RHC8_PLAIO	07rhc8 plasmodium
76	32	74.4	1282	2 05JH54_PYROO	05jh54 pyrococcus
77	32	74.4	1297	2 04YX18_PLAEB	04yx18 plasmodium
78	32	74.4	3228	2 06D920_ERWCT	06d920 erwina car
79	31	72.1	57	2 08E4W8_STRAS	08e4w8 streptococc
80	31	72.1	96	2 09KX93_ECO57	09kx93 escherichia
81	31	72.1	120	1 CBIX_STUTO	0975b6 sulfolobus
82	31	72.1	127	2 07MND5_ECOLI	07mnd5 escherichia
83	31	72.1	152	2 083LK9_SHITL	083lk9 shigella fl
84	31	72.1	164	1 YCDH_ECO57	08x40 escherichia
85	31	72.1	164	1 YCDH_ECO57	075833 escherichia
86	31	72.1	167	2 0678B6_VIUIU	0678b6 lymphocysti
87	31	72.1	184	2 08FJ45_ECOL6	08fj45 escherichia
88	31	72.1	198	2 04HRC8_CAMCO	04hrc8 campylobact
89	31	72.1	225	2 061X71_METNP	061x71 methanococc
90	31	72.1	248	2 05H834_STRSU	05h834 streptococc
91	31	72.1	256	2 04RH45_TETNG	04rh45 tetradon n
92	31	72.1	267	2 051AC8_ENTHI	051ac8 entamoeba h
93	31	72.1	267	2 06NTJ8_XENLA	06ntj8 xenopus lae
94	31	72.1	269	2 06NTJ8_XENLA	06ntj8 xenopus lae
95	31	72.1	294	2 07VID7_HEIAP	07vid7 helicobacte
96	31	72.1	302	2 07PUB8_ANOGA	07pub8 anopheles g
97	31	72.1	311	2 064YN4_BACRA	064yn4 bacteroides
98	31	72.1	313	2 04Z5Z2_PLAEB	04z5z2 plasmodium
99	31	72.1	343	2 09VYJ4_DROBE	09vyj4 dirosophila
100	31	72.1	344	1 ARGC_GEOKA	0511v5 geobacillus
101	31	72.1	345	1 ARGC_BACST	007906 bacillus st
102	31	72.1	352	2 05ATX9_EMENT	05atx9 aspergillus
103	31	72.1	364	1 Y2027_AQUAE	067821 aquifex aeo
104	31	72.1	380	2 08RZ49_ORYSA	08rz49 oryza sativ

105	31	72.1	394	2	Q9V36	DROME	Q9V36	drosophila
106	31	72.1	399	2	Q67R4	SVIRU	Q67R4	lymphocysti
107	31	72.1	408	2	Q7WH9	HABPU	Q7WH9	haemophilus
108	31	72.1	412	2	Q4WAL	ASPPU	Q4WAL	aspergillus
109	31	72.1	421	2	Q7X28	SPLAN	Q7X28	gemmatae sp.
110	31	72.1	428	2	P3843	TOBAC	P3843	nicotiana t
111	31	72.1	429	2	Q9LEB3	NICPL	Q9LEB3	nicotiana p
112	31	72.1	432	2	Q9USPO	LAMPF	Q9USPO	lampecta fi
113	31	72.1	433	2	Q5BW6	SCHUA	Q5BW6	schistosoma
114	31	72.1	432	2	Q6UING	BIOOL	Q6UING	biomphali
115	31	72.1	436	2	Q7YMS	SCAUD	Q7YMS	bacteriophia
116	31	72.1	444	2	Q5AKY3	CANAL	Q5AKY3	canidia alb
117	31	72.1	460	2	Q8DY6	STRAS	Q8DY6	streptococ
118	31	72.1	460	2	Q8HKAT	SGAST	Q8HKAT	robassera e
119	31	72.1	478	2	Q4955	TOBAC	Q4955	nicotiana t
120	31	72.1	508	2	Q72FW2	DESVH	Q72FW2	desulfovibr
121	31	72.1	515	2	Q4WA88	ASPPU	Q4WA88	aspergillus
122	31	72.1	521	2	Q9MD18	SCBOB	Q9MD18	scenedesmus
123	31	72.1	529	2	Q4K961	PSRPS	Q4K961	pseudomonas
124	31	72.1	534	1	FM03	MOUSE	FM03	mus musculus
125	31	72.1	549	2	Q4WKJ3	ASPPU	Q4WKJ3	aspergillus
126	31	72.1	557	2	Q4UJZ7	RICFE	Q4UJZ7	ricfetsia
127	31	72.1	570	2	Q9C866	ARATH	Q9C866	arabidopsis
128	31	72.1	577	2	Q5AZP2	EMENT	Q5AZP2	aspergillus
129	31	72.1	590	2	Q81LUS	PLAF7	Q81LUS	plasmodium
130	31	72.1	599	2	Q7R2B0	GIALA	Q7R2B0	giardia lam
131	31	72.1	629	2	Q6XQ15	DESPS	Q6XQ15	desulfohal
132	31	72.1	635	2	Q9C7B0	ARATH	Q9C7B0	arabidopsis
133	31	72.1	638	2	Q9LHBI	ARATH	Q9LHBI	arabidopsis
134	31	72.1	701	2	Q54LQ5	DICDI	Q54LQ5	dictyostell
135	31	72.1	730	2	Q6PEH8	BRARE	Q6PEH8	brachydanio
136	31	72.1	741	2	Q8H0H2	TOBAC	Q8H0H2	nicotiana t
137	31	72.1	753	2	Q5CTG5	CRYPV	Q5CTG5	cryptospori
138	31	72.1	777	2	Q6N8N6	RIOPA	Q6N8N6	rhodopsedu
139	31	72.1	777	2	Q8CANG	MOUSE	Q8CANG	mus musculus
140	31	72.1	791	1	ELG1	YEAST	ELG1	saccharomyc
141	31	72.1	794	1	SECI18	CANAL	SECI18	canidia alb
142	31	72.1	805	2	Q5CTU6	CRYPV	Q5CTU6	cryptospori
143	31	72.1	805	2	Q5CH66	CRYPH	Q5CH66	cryptospori
144	31	72.1	808	2	Q94A27	ARATH	Q94A27	arabidopsis
145	31	72.1	816	2	Q9LJG4	ARATH	Q9LJG4	arabidopsis
146	31	72.1	816	2	Q9LJG4	ARATH	Q9LJG4	arabidopsis
147	31	72.1	1069	1	ENTK	MOUSE	ENTK	mus musculus
148	31	72.1	1346	2	Q72A44	DESVH	Q72A44	desulfovibr
149	31	72.1	1657	2	Q7F6X2	MIMIV	Q7F6X2	mimivirius
150	31	72.1	2221	2	Q81259	PLAF7	Q81259	plasmodium
151	31	72.1	3580	2	Q65NK5	BACLD	Q65NK5	bacillus 11
152	31	72.1	3582	2	Q66069	BACLD	Q66069	bacillus 11
153	31	72.1	3583	2	Q45295	BACLI	Q45295	schistosac
154	31	72.1	3655	1	YAMB	SCHPO	YAMB	schistosoma
155	31	69.8	47	2	Q9X1J2	NEIMB	Q9X1J2	neisseria m
156	30	69.8	57	2	Q7R6E1	GIALA	Q7R6E1	giardia lam
157	30	69.8	70	2	Q5KK15	GEOXA	Q5KK15	geobacillus
158	30	69.8	81	2	Q9ZRL6	WHEAT	Q9ZRL6	tritricum ae
159	30	69.8	88	2	Q66300	WHEAT	Q66300	tritricum ae
160	30	69.8	92	2	P93686	SECCE	P93686	secale cere
161	30	69.8	109	2	Q8H587	ORYSA	Q8H587	oryza sativ
162	30	69.8	119	2	Q6BUFI	DEBNA	Q6BUFI	debaryomyce
163	30	69.8	122	2	Q6NDAP	RIOPA	Q6NDAP	rhodopsedu
164	30	69.8	134	1	YFFE	SCHPO	YFFE	schistosac
165	30	69.8	136	2	Q18208	CABEL	Q18208	caenorhabdi
166	30	69.8	152	1	PSAL	GUTTH	PSAL	guillardi
167	30	69.8	167	1	PBL	ECOS7	PBL	escherichia
168	30	69.8	172	2	Q4P7R8	USPMA	Q4P7R8	uselliago ma
169	30	69.8	181	2	Q5Y2F4	9H1V1	Q5Y2F4	human immun
170	30	69.8	183	2	Q8XY53	RALSO	Q8XY53	ralesonia s
171	30	69.8	191	2	Q8D7F7	VIBUV	Q8D7F7	vibrio vuln
172	30	69.8	192	2	Q9N3H6	CABEL	Q9N3H6	caenorhabdi
173	30	69.8	195	2	Q7MEG7	VIEVY	Q7MEG7	vibrio vuln
174	30	69.8	207	2	Q80124	9CAUD	Q80124	bacterioph
175	30	69.8	210	2	Q7ZNB9	9H1V1	Q7ZNB9	human immun
176	30	69.8	215	2	Q5DNB5	9H1V1	Q5DNB5	leptothrych
177	30	69.8	223	2	Q9AAA7	_CAUCR	Q9AAA7	caulobacter
178	30	69.8	229	2	Q9K0B6	NEIMB	Q9K0B6	neisseria m
179	30	69.8	231	2	Q817L8	CABEL	Q817L8	caenorhabdi
180	30	69.8	230	2	Q9JVC1	NEIMA	Q9JVC1	neisseria m
181	30	69.8	245	2	Q6B839	CARMV	Q6B839	carriation m
182	30	69.8	245	2	Q9DJV5	CARMV	Q9DJV5	carriation m
183	30	69.8	245	2	Q9G6X8	CARMV	Q9G6X8	carriation m
184	30	69.8	249	2	Q6SE99	9CAUD	Q6SE99	lactobacilli
185	30	69.8	249	2	Q5EPMO	LACIO	Q5EPMO	lactobacilli
186	30	69.8	273	2	Q8VTW7	LEPIN	Q8VTW7	leptococci
187	30	69.8	274	2	Q6ZFJ0	ORYSA	Q6ZFJ0	oryza sativ
188	30	69.8	280	2	Q5LEM3	ENTHI	Q5LEM3	entamoeba h
189	30	69.8	282	2	Q4G2U4	LYCPM	Q4G2U4	lycopersico
190	30	69.8	282	2	Q4G2U2	LYCPM	Q4G2U2	lycopersico
191	30	69.8	282	2	Q4G2U1	LYCPM	Q4G2U1	lycopersico
192	30	69.8	282	2	Q4G2U1	LYCPM	Q4G2U1	lycopersico
193	30	69.8	282	2	Q4G2U1	LYCPM	Q4G2U1	lycopersico
194	30	69.8	292	2	Q7CZNO	AGRTS	Q7CZNO	agrobacteri
195	30	69.8	294	2	Q79RC5	FRATT	Q79RC5	francisella
196	30	69.8	296	2	Q9R2B2	DEIRA	Q9R2B2	deinococcus
197	30	69.8	297	2	Q8Y5H8	LISMO	Q8Y5H8	listeria mo
198	30	69.8	297	2	Q923T4	LISIN	Q923T4	listeria in
199	30	69.8	300	2	Q74BF8	GROSL	Q74BF8	geobacter s
200	30	69.8	304	2	Q8S390	AMAMP	Q8S390	amarantus
201	30	69.8	304	2	Q7IOF2	AMACA	Q7IOF2	amarantus
202	30	69.8	304	2	Q6YXK3	AMACA	Q6YXK3	amarantus
203	30	69.8	313	2	Q817L9	CAEHL	Q817L9	caenorhabdi
204	30	69.8	320	2	Q6AGS6	LEIXX	Q6AGS6	leifsonia x
205	30	69.8	320	2	Q84684	9VIRU	Q84684	peanut chlo
206	30	69.8	321	1	GUNI	STRHA	GUNI	streptomyce
207	30	69.8	354	2	Q5WJH2	BACSK	Q5WJH2	bacillus c1
208	30	69.8	357	2	Q9CDG5	IACIA	Q9CDG5	lactococcus
209	30	69.8	361	2	Q6DLA4	CIOIN	Q6DLA4	ciona intes
210	30	69.8	361	2	Q51965	BACFEN	Q51965	bacteroides
211	30	69.8	366	2	Q6MMB1	BDEBA	Q6MMB1	bdellovibri
212	30	69.8	367	2	Q9T212	CABEL	Q9T212	caenorhabdi
213	30	69.8	368	2	Q61CM8	CABEL	Q61CM8	caenorhabdi
214	30	69.8	369	2	Q81NM6	9BURK	Q81NM6	myxine glut
215	30	69.8	373	2	Q4ZPP7	PSSEY	Q4ZPP7	pseudomonas
216	30	69.8	374	2	Q87XK8	PSSEY	Q87XK8	pseudomonas
217	30	69.8	374	2	Q62ER6	BURPS	Q62ER6	burkholderi
218	30	69.8	377	2	Q63Y99	BURPS	Q63Y99	burkholderi
219	30	69.8	379	2	Q4WMS3	ASPPU	Q4WMS3	aspergillus
220	30	69.8	383	2	Q7VX55	BORR	Q7VX55	borderella
221	30	69.8	383	2	Q7W821	BORR	Q7W821	borderella
222	30	69.8	392	2	Q7W821	BORR	Q7W821	borderella
223	30	69.8	402	2	Q9KDP4	BACDH	Q9KDP4	bacillus ha
224	30	69.8	402	2	Q8CHN1	STAP	Q8CHN1	staphylococ
225	30	69.8	402	2	Q8CHN1	STAP	Q8CHN1	staphylococ
226	30	69.8	402	2	Q8CHN1	STAP	Q8CHN1	staphylococ
227	30	69.8	402	2	Q8CHN1	STAP	Q8CHN1	staphylococ
228	30	69.8	408	1	YOL7	ROURE	YOL7	roure
229	30	69.8	419	2	Q61M63	CABER	Q61M63	caenorhabdi
230	30	69.8	419	2	Q5Z862	ORYSA	Q5Z862	oryza sativ
231	30	69.8	417	2	Q5YX04	NOCRA	Q5YX04	nocardia fa
232	30	69.8	428	2	Q9R667	LYCPS	Q9R667	lycopersico
233	30	69.8	443	2	Q8BHW2	SHRON	Q8BHW2	shewanella
234	30	69.8	443	2	Q8CRP9	BRARE	Q8CRP9	brachydanio
235	30	69.8	457	1	Q51GTF	ENTHI	Q51GTF	entamoeba h
236	30	69.8	457	1	Q51GTF	ENTHI	Q51GTF	entamoeba h
237	30	69.8	457	1	Q51GTF	ENTHI	Q51GTF	entamoeba h
238	30	69.8	474	2	Q8YR65	ANASP	Q8YR65	anopheles g
239	30	69.8	474	2	Q8YR65	ANASP	Q8YR65	anopheles g
240	30	69.8	484	2	Q8SUXO	TEYNG	Q8SUXO	tetradon n
241	30	69.8	484	2	Q8SUXO	TEYNG	Q8SUXO	tetradon n
242	30	69.8	488	2	Q8SUXO	TEYNG	Q8SUXO	tetradon n
243	30	69.8	488	2	Q8SUXO	TEYNG	Q8SUXO	tetradon n
244	30	69.8	488	2	Q8SUXO	TEYNG	Q8SUXO	tetradon n
245	30	69.8	488	2	Q8SUXO	TEYNG	Q8SUXO	tetradon n
246	30	69.8	488	2	Q8SUXO	TEYNG	Q8SUXO	tetradon n
247	30	69.8	501	1	NBOW	BUCHE	NBOW	buchnera ap
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256	30	69.8	513	2	Q97018	STUTO	Q97018	staphylococ
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:21 ; Search time 17.449 Seconds
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 100% summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	33	76.7	819	2	US-09-328-352-4650 Sequence 4650, Ap
2	32	74.4	124	2	US-09-663-600A-91 Sequence 91, Appl
3	32	74.4	124	2	US-09-663-600A-185 Sequence 185, App
4	32	74.4	124	2	US-09-663-600A-215 Sequence 215, App
5	32	74.4	124	2	US-09-621-976-14 Sequence 14, Appl
6	32	74.4	124	2	US-09-492-709A-337 Sequence 337, Appl
7	31	72.1	194	2	US-09-270-767-33892 Sequence 33892, A
8	31	72.1	194	2	US-09-270-767-49109 Sequence 49109, A
9	31	72.1	303	2	US-09-248-796A-14416 Sequence 14416, A
10	31	72.1	514	2	US-09-543-681A-4255 Sequence 4255, Ap
11	30	69.8	126	2	US-09-232-290-35 Sequence 35, Appl
12	30	69.8	134	2	US-09-732-210-1742 Sequence 1742, Ap
13	30	69.8	242	2	US-09-270-767-47078 Sequence 47078, A
14	30	69.8	265	2	US-09-540-336-3285 Sequence 3285, Ap
15	30	69.8	266	2	US-09-270-767-31861 Sequence 31861, A
16	30	69.8	356	2	US-09-107-532A-4245 Sequence 4245, Ap
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18	30	69.8	366	2	US-09-328-352-7292 Sequence 7292, Ap
19	30	69.8	377	2	US-09-107-532A-4318 Sequence 4318, Ap
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OM protein - protein search, using sw model

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86.753 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1867569

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	33	76.7	170	4	US-10-282-122A-56358
6	33	76.7	189	4	US-10-424-599-144524
7	33	76.7	656	4	US-10-767-701-46396
8	32	74.4	82	4	US-10-437-963-158329
9	32	74.4	97	4	US-10-437-963-200385
10	32	74.4	124	3	US-09-978-360A-697
11	32	74.4	124	3	US-09-978-360A-727
12	32	74.4	124	4	US-10-319-763-91
13	32	74.4	124	4	US-10-319-763-185
14	32	74.4	124	4	US-10-319-763-215
15	32	74.4	124	4	US-10-264-237-2204
16	32	74.4	124	5	US-10-617-316-139
17	32	74.4	124	5	US-10-617-316-209
18	32	74.4	124	5	US-10-369-493-19705
19	32	74.4	296	3	US-09-912-020-337
20	32	74.4	296	3	US-10-282-122A-42616
21	32	74.4	296	5	US-10-771-241-337
22	32	74.4	323	4	US-10-335-977-5007
23	32	74.4	399	5	US-10-954-778-15
24	32	74.4	425	4	US-10-437-963-158681
25	32	74.4	444	4	US-10-156-761-13243
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38	31	72.1	428	4	US-10-062-254-372	Sequence 372, App
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107	30	69.8	2969	3	US-09-738-626-4434	Sequence 4434, Ap	180	29	67.4	548	4	US-10-437-963-171491	Sequence 171491, A
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134	29	67.4	277	4	US-10-732-923-19096	Sequence 47150, A	207	29	67.4	1140	6	US-10-108-605-293	Sequence 41646, A
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154	29	67.4	407	4	US-10-437-963-156447	Sequence 156447,	228	29	67.4	68	4	US-10-424-599-237298	Sequence 237298, A
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:04 ; Search time 7.89796 Seconds
(without alignments)
48,418 Million cell updates/sec

Title: US-10-067-484-3
Perfect score: 43
Sequence: 1 XYGIVQFNR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA.New.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	32	74.4	124	5	US-09-978-360A-727
5	32	74.4	291	7	US-11-188-298-3698
6	32	74.4	751	7	US-11-052-554A-109
7	32	74.4	949	6	US-10-506-454-104
8	31	72.1	240	6	US-10-467-657-7756
9	31	72.1	3580	6	US-10-510-941-14
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:40:47 ; Search time 70.5714 Seconds

(Without alignments)
43.582 Million cell updates/sec

Title: US-10-067-484-4

Perfect score: 33

Sequence: 1 FVFXSTRK 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

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- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	30	90.9	218	4	ADL04980
4	29	87.9	85	6	ABP80721
5	29	87.9	85	6	ABP80255
6	29	87.9	284	8	ADK92845
7	29	87.9	329	7	ADK94153
8	29	87.9	358	6	ABU34617
9	29	87.9	359	2	AAW46752
10	29	87.9	364	6	ABP57038
11	29	87.9	369	6	ABU3822
12	29	87.9	373	6	ABP57037
13	29	87.9	373	6	ABP57039
14	29	87.9	373	6	ABP57036
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16	29	87.9	373	6	ABU36891
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24	28	84.8	40	4	AAW48125

25	28	84.8	73	4	AAW17792
26	28	84.8	73	4	ABB36817
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28	28	84.8	73	4	ABB31596
29	28	84.8	73	4	ABB22140
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31	28	84.8	73	4	AAW57558
32	28	84.8	73	4	ABG51661
33	28	84.8	73	4	AAW05439
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35	28	84.8	86	4	AAO12999
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91	28	84.8	395	6	ABU04615
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ABU25808	Protein e
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ADW98761	Borrelia
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ABU04617	Human exp
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104	28	84.8	493	2	AAW89151	AAW89151	Human CD4	177	27	81.8	69	5	ABF11245	ABF11245	Human ORF
105	28	84.8	493	3	AAV96140	AAV96140	Human epi	178	27	81.8	85	7	ABF03374	ABF03374	Human ORF
106	28	84.8	493	4	AAU02449	AAU02449	Human epi	179	27	81.8	86	4	AAU68124	AAU68124	Human ORF
107	28	84.8	493	5	AAU09123	AAU09123	Haemato	180	27	81.8	88	6	AAU65668	AAU65668	Human ORF
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110	28	84.8	493	6	ABU04639	ABU04639	Human exp	183	27	81.8	91	4	ADP30200	ADP30200	Human sec
111	28	84.8	493	6	ABU04631	ABU04631	Human exp	184	27	81.8	106	5	ADP30200	ADP30200	Human sec
112	28	84.8	493	6	ABU04633	ABU04633	Human exp	185	27	81.8	132	3	ABE21153	ABE21153	Human ORF
113	28	84.8	493	6	ABU04612	ABU04612	Human exp	186	27	81.8	138	3	ABE21153	ABE21153	Human ORF
114	28	84.8	493	6	ABU04613	ABU04613	Human exp	187	27	81.8	161	8	ABE18091	ABE18091	Human ORF
115	28	84.8	493	6	ABU04635	ABU04635	Human exp	188	27	81.8	161	8	ADK95357	ADK95357	Human ORF
116	28	84.8	493	6	ABU04613	ABU04613	Human exp	189	27	81.8	166	4	AAE61827	AAE61827	Plant full
117	28	84.8	493	8	ADL93507	ADL93507	Human CD4	190	27	81.8	166	4	ADT28662	ADT28662	Human int
118	28	84.8	493	8	ADU049375	ADU049375	Human CD4	191	27	81.8	177	4	ABE70705	ABE70705	Human int
119	28	84.8	493	8	ADU049375	ADU049375	Human CD4	192	27	81.8	191	4	AAU30717	AAU30717	Human int
120	28	84.8	493	8	ABE87764	ABE87764	Human CD4	193	27	81.8	259	8	ADK46373	ADK46373	Human int
121	28	84.8	518	5	AAO17871	AAO17871	Pylin dom	194	27	81.8	271	6	AAU00926	AAU00926	S. pneumo
122	28	84.8	535	8	ABM83594	ABM83594	Human dia	195	27	81.8	277	4	AAE96795	AAE96795	Putative
123	28	84.8	535	8	ABP72424	ABP72424	Human myo	196	27	81.8	285	2	AAE52270	AAE52270	H. pylori
124	28	84.8	608	6	ABP72424	ABP72424	Human CD4	197	27	81.8	285	8	ADR96088	ADR96088	Novel S.
125	28	84.8	642	4	AAU25640	AAU25640	Human pro	198	27	81.8	285	6	AAE59958	AAE59958	Streptoco
126	28	84.8	675	6	ABU04618	ABU04618	Human exp	199	27	81.8	304	3	ABM73077	ABM73077	Streptoco
127	28	84.8	676	6	ABU04602	ABU04602	Human exp	200	27	81.8	310	3	AAE12765	AAE12765	Streptoco
128	28	84.8	676	6	ABU04652	ABU04652	Human exp	201	27	81.8	310	7	AAE12765	AAE12765	Streptoco
129	28	84.8	691	8	ABU04621	ABU04621	Human exp	202	27	81.8	310	7	ADU30632	ADU30632	Streptoco
130	28	84.8	691	8	ADU30390	ADU30390	Human myo	203	27	81.8	310	7	ADU30632	ADU30632	Streptoco
131	28	84.8	699	6	ABU04647	ABU04647	Human exp	204	27	81.8	328	2	ADL1863	ADL1863	Plant yie
132	28	84.8	699	6	ABU04647	ABU04647	Human exp	205	27	81.8	328	2	AAE5486	AAE5486	Plant tra
133	28	84.8	699	6	ABU04614	ABU04614	Human exp	206	27	81.8	332	3	AAE12763	AAE12763	Plant tra
134	28	84.8	699	6	ABU04608	ABU04608	Human exp	207	27	81.8	339	3	AAE14313	AAE14313	Human sec
135	28	84.8	699	7	ADD90596	ADD90596	Human CD4	208	27	81.8	339	3	AAE85235	AAE85235	Human sec
136	28	84.8	699	9	ADV73230	ADV73230	Human CD4	209	27	81.8	342	3	AAE85235	AAE85235	Human sec
137	28	84.8	699	9	ADV73230	ADV73230	Human CD4	210	27	81.8	361	3	AAE85235	AAE85235	Human sec
138	28	84.8	699	9	ADV73230	ADV73230	Human CD4	211	27	81.8	366	6	AAE85235	AAE85235	Human sec
139	28	84.8	700	4	AAV97579	AAV97579	Human CD4	212	27	81.8	367	7	AAE85235	AAE85235	Human sec
140	28	84.8	700	4	AAV97579	AAV97579	Human CD4	213	27	81.8	367	7	AAE85235	AAE85235	Human sec
141	28	84.8	700	7	ADD90594	ADD90594	Human CD4	214	27	81.8	370	9	AAE85235	AAE85235	Human sec
142	28	84.8	700	7	ADD90594	ADD90594	Human CD4	215	27	81.8	379	9	AAE85235	AAE85235	Human sec
143	28	84.8	719	6	ABU04604	ABU04604	Human exp	216	27	81.8	409	7	ABM88540	ABM88540	Human mem
144	28	84.8	719	6	ABU04604	ABU04604	Human exp	217	27	81.8	416	8	ADK87436	ADK87436	Human mem
145	28	84.8	742	4	ABU04650	ABU04650	Human exp	218	27	81.8	458	4	ADK87436	ADK87436	Human mem
146	28	84.8	742	4	ABU04653	ABU04653	Human exp	219	27	81.8	458	7	ADK87436	ADK87436	Human mem
147	28	84.8	742	4	ABU04653	ABU04653	Human exp	220	27	81.8	458	7	ADK87436	ADK87436	Human mem
148	28	84.8	742	4	ABU04653	ABU04653	Human exp	221	27	81.8	459	5	ADK87436	ADK87436	Human mem
149	28	84.8	742	4	ABU04653	ABU04653	Human exp	222	27	81.8	459	7	ADK87436	ADK87436	Human mem
150	28	84.8	742	4	ABU04653	ABU04653	Human exp	223	27	81.8	474	8	ADK87436	ADK87436	Human mem
151	28	84.8	742	4	ABU04653	ABU04653	Human exp	224	27	81.8	476	8	ADK87436	ADK87436	Human mem
152	28	84.8	742	4	ABU04653	ABU04653	Human exp	225	27	81.8	478	4	ADK87436	ADK87436	Human mem
153	28	84.8	742	4	ABU04653	ABU04653	Human exp	226	27	81.8	478	5	ADK87436	ADK87436	Human mem
154	28	84.8	742	4	ABU04653	ABU04653	Human exp	227	27	81.8	478	5	ADK87436	ADK87436	Human mem
155	28	84.8	742	4	ABU04653	ABU04653	Human exp	228	27	81.8	478	6	ADK87436	ADK87436	Human mem
156	28	84.8	742	4	ABU04653	ABU04653	Human exp	229	27	81.8	478	6	ADK87436	ADK87436	Human mem
157	28	84.8	742	4	ABU04653	ABU04653	Human exp	230	27	81.8	478	6	ADK87436	ADK87436	Human mem
158	28	84.8	742	4	ABU04653	ABU04653	Human exp	231	27	81.8	478	6	ADK87436	ADK87436	Human mem
159	28	84.8	742	4	ABU04653	ABU04653	Human exp	232	27	81.8	478	6	ADK87436	ADK87436	Human mem
160	28	84.8	742	4	ABU04653	ABU04653	Human exp	233	27	81.8	478	6	ADK87436	ADK87436	Human mem
161	28	84.8	742	4	ABU04653	ABU04653	Human exp	234	27	81.8	478	6	ADK87436	ADK87436	Human mem
162	28	84.8	742	4	ABU04653	ABU04653	Human exp	235	27	81.8	478	6	ADK87436	ADK87436	Human mem
163	28	84.8	742	4	ABU04653	ABU04653	Human exp	236	27	81.8	478	6	ADK87436	ADK87436	Human mem
164	28	84.8	742	4	ABU04653	ABU04653	Human exp	237	27	81.8	478	6	ADK87436	ADK87436	Human mem
165	28	84.8	742	4	ABU04653	ABU04653	Human exp	238	27	81.8	478	6	ADK87436	ADK87436	Human mem
166	28	84.8	742	4	ABU04653	ABU04653	Human exp	239	27	81.8	478	6	ADK87436	ADK87436	Human mem
167	28	84.8	742	4	ABU04653	ABU04653	Human exp	240	27	81.8	478	6	ADK87436	ADK87436	Human mem
168	28	84.8	742	4	ABU04653	ABU04653	Human exp	241	27	81.8	478	6	ADK87436	ADK87436	Human mem
169	28	84.8	742	4	ABU04653	ABU04653	Human exp	242	27	81.8	478	6	ADK87436	ADK87436	Human mem
170	28	84.8	742	4	ABU04653	ABU04653	Human exp	243	27	81.8	478	6	ADK87436	ADK87436	Human mem

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:12 ; Search time 6.42857 Seconds
(without alignments)
104.769 Million cell updates/sec

Title: US-10-067-484-4

Perfect score: 33
Sequence: 1 FYXFSRK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

1: PIR 80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	116	2	SS0449
2	30	90.9	201	2	G64013
3	29	87.9	94	2	H69748
4	29	87.9	222	2	T30423
5	29	87.9	258	2	T45991
6	29	87.9	373	2	B70673
7	29	87.9	373	2	T34126
8	29	87.9	384	2	H87118
9	28	84.8	230	2	H70114
10	28	84.8	242	2	T16349
11	28	84.8	285	2	G72401
12	28	84.8	361	2	JH0417
13	28	84.8	395	2	I77371
14	28	84.8	426	2	JH0518
15	28	84.8	464	2	A47442
16	28	84.8	468	2	G70417
17	28	84.8	493	2	S13530
18	28	84.8	508	2	T22626
19	28	84.8	699	2	I37369
20	28	84.8	742	2	A47195
21	27	81.8	245	2	T33840
22	27	81.8	247	2	H64524
23	27	81.8	248	2	B97794
24	27	81.8	271	2	A85065
25	27	81.8	271	2	G97932
26	27	81.8	277	2	E75187
27	27	81.8	277	2	D71220
28	27	81.8	297	2	A81381
29	27	81.8	304	2	T05587

30	27	81.8	328	2	A71981
31	27	81.8	331	2	T20916
32	27	81.8	338	2	I40448
33	27	81.8	369	2	D90351
34	27	81.8	372	2	T25621
35	27	81.8	396	2	T24576
36	27	81.8	396	2	T39676
37	27	81.8	431	2	T20263
38	27	81.8	462	2	B88613
39	27	81.8	488	2	G81295
40	27	81.8	510	2	I39930
41	27	81.8	520	2	G88846
42	27	81.8	572	2	T47219
43	27	81.8	576	2	T25375
44	27	81.8	656	2	A72428
45	27	81.8	656	2	E72379
46	27	81.8	661	2	G72316
47	27	81.8	819	2	UC7240
48	27	81.8	827	1	COBYD1
49	27	81.8	835	2	JC6140
50	27	81.8	1047	2	T46599
51	27	81.8	1557	2	T28811
52	27	81.8	1770	2	A71517
53	27	81.8	2824	2	T22759
54	26	78.8	31	2	E82329
55	26	78.8	31	2	T11156
56	26	78.8	109	2	S58781
57	26	78.8	125	2	T03359
58	26	78.8	128	2	AC1150
59	26	78.8	128	2	AD1509
60	26	78.8	146	2	B95205
61	26	78.8	181	2	T23333
62	26	78.8	190	2	F97812
63	26	78.8	206	2	T35415
64	26	78.8	206	2	C83590
65	26	78.8	207	2	B69124
66	26	78.8	220	2	S44808
67	26	78.8	229	2	A37775
68	26	78.8	229	2	C82975
69	26	78.8	229	2	H82388
70	26	78.8	226	2	AI0142
71	26	78.8	250	2	T25632
72	26	78.8	253	2	A88955
73	26	78.8	264	2	B71721
74	26	78.8	266	2	D97719
75	26	78.8	282	2	T07182
76	26	78.8	287	2	H83306
77	26	78.8	309	2	D70464
78	26	78.8	318	2	T20617
79	26	78.8	360	1	C8EBDT
80	26	78.8	364	2	CEEBDT
81	26	78.8	364	2	AC0549
82	26	78.8	364	2	G90682
83	26	78.8	364	2	C85533
84	26	78.8	365	2	B70435
85	26	78.8	378	2	D83945
86	26	78.8	382	2	G86791
87	26	78.8	405	2	G86848
88	26	78.8	408	2	C95100
89	26	78.8	408	2	E97968
90	26	78.8	408	2	AE1376
91	26	78.8	408	2	AG1745
92	26	78.8	413	2	D89857
93	26	78.8	454	2	A99470
94	26	78.8	461	2	C69353
95	26	78.8	465	2	A56679
96	26	78.8	482	2	A10554
97	26	78.8	482	2	E90688
98	26	78.8	482	2	T46944
99	26	78.8	482	2	A85539
100	26	78.8	482	2	G64771
101	26	78.8	487	2	I40654
102	26	78.8	487	1	

DNA transformation
hypothetical prote
conserved hypotet
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probable yeast cel
hypothetical prote
protein T27E9.5 [1
cytochrome-c oxida
replication protei
protein T12A7.2 [1
amino acid transpo
hypothetical prote
methyl-accepting c
methyl-accepting c
two-pore calcium c
RED1 protein - yea
cell surface-assoc
glutamate dehydrog
hypothetical prote
hypothetical prote
hypothetical prote
ATPase 8 - hardbac
probable membrane
gene e8 protein -
hypothetical prote
hypothetical prote
conserved domain p
hypothetical prote
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F4489.9 protein -
phoB protein - pse
two-component resp
DNA-binding respon
probable membrane
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protein K04F1.1 [1
probable signal pe
signal peptidase I
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probable RNA-bind
thiamin biosynthes
probable oxidoredu
thiamin biosynthes
probable oxidoredu
yijk protein - Esc
60K inner membrane

175	174	173	172	171	170	169	168	167	166	165	164	163	162	161	160	159	158	157	156	155	154	153	152	151	150	149	148	147	146	145	144	143	142	141	140	139	138	137	136	135	134	133	132	131	130	129	128	127	126	125	124	123	122	121	120	119	118	117	116	115	114	113	112	111	110	109	108	107	106	105	104	103	102	101	100	99	98	97	96	95	94	93	92	91	90	89	88	87	86	85	84	83	82	81	80	79	78	77	76	75	74	73	72	71	70	69	68	67	66	65	64	63	62	61	60	59	58	57	56	55	54	53	52	51	50	49	48	47	46	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	0
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175	174	173	172	171	170	169	168	167	166	165	164	163	162	161	160	159	158	157	156	155	154	153	152	151	150	149	148	147	146	145	144	143	142	141	140	139	138	137	136	135	134	133	132	131	130	129	128	127	126	125	124	123	122	121	120	119	118	117	116	115	114	113	112	111	110	109	108	107	106	105	104	103	102	101	100	99	98	97	96	95	94	93	92	91	90	89	88	87	86	85	84	83	82	81	80	79	78	77	76	75	74	73	72	71	70	69	68	67	66	65	64	63	62	61	60	59	58	57	56	55	54	53	52	51	50	49	48	47	46	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	0
175	174	173	172	171	170	169	168	167	166	165	164	163	162	161	160	159	158	157	156	155	154	153	152	151	150	149	148	147	146	145	144	143	142	141	140	139	138	137	136	135	134	133	132	131	130	129	128	127	126	125	124	123	122	121	120	119	118	117	116	115	114	113	112	111	110	109	108	107	106	105	104	103	102	101	100	99	98	97	96	95	94	93	92	91	90	89	88	87	86	85	84	83	82	81	80	79	78	77	76	75	74	73	72	71	70	69	68	67	66	65	64	63	62	61	60	59	58	57	56	55	54	53	52	51	50	49	48	47	46	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	0
175	174	173	172	171	170	169	168	167	166	165	164	163	162	161	160	159	158	157	156	155	154	153	152	151	150	149	148	147	146	145	144	143	142	141	140	139	138	137	136	135	134	133	132	131	130	129	128	127	126	125	124	123	122	121	120	119	118	117	116	115	114	113	112	111	110	109	108	107	106	105	104	103	102	101	100	99	98	97	96	95	94	93	92	91	90	89	88	87	86	85	84	83	82	81	80	79	78	77	76	75	74	73	72	71	70	69	68	67	66	65	64	63	62	61	60	59	58	57	56	55	54	53	52	51	50	49	48	47	46	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	0
175	174	173	172	171	170	169	168	167	166	165	164	163	162	161	160	159	158	157	156	155	154	153	152	151	150	149	148	147	146	145	144	143	142	141	140	139	138	137	136	135	134	133	132	131	130	129	128	127	126	125	124	123	122	121	120	119	118	117	116	115	114	113	112	111	110	109	108	107	106	105	104	103	102	101	100	99	98	97	96	95	94	93	92</																																																																																												

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:05 ; Search time 38.1429 Seconds
(without alignments)
129.479 Million cell updates/sec

Title: US-10-067-484-4
Perfect score: 33
Sequence: 1 FXXFSTK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	41	2	091FZ4 IRV6
2	32	97.0	108	2	06EB60 CAMJE
3	32	97.0	281	2	061VH7 CAEBR
4	32	97.0	416	2	04HD92 CAMCO
5	32	97.0	615	2	081JDP PLAF7
6	32	97.0	1751	2	054T12 DICDI
7	30	90.9	60	2	08F8P3 LBPIN
8	30	90.9	116	1	YEB0_YEAST
9	30	90.9	199	2	087NM8 VIBPA
10	30	90.9	201	1	Y787_HABIN
11	30	90.9	207	2	04QWB2 HAE18
12	30	90.9	473	2	0600W4 MYCHY
13	30	90.9	477	2	0642R1 XENLA
14	30	90.9	623	2	0517H8_ENTHI
15	29	87.9	30	2	041PV1 PLABE
16	29	87.9	94	1	YBFE_BACSU
17	29	87.9	100	2	065XA7 ORYSA
18	29	87.9	129	2	041450 STAHJ
19	29	87.9	202	2	061PY2 PHOPR
20	29	87.9	207	2	063BG4_BACCZ
21	29	87.9	209	2	050SE7_ENTHI
22	29	87.9	209	2	05NT08_ENTHI
23	29	87.9	209	2	06HIX3_BACCH
24	29	87.9	209	2	081OL8_BACAN
25	29	87.9	222	2	09YMO2_NPVLD
26	29	87.9	224	2	08VSW2_STAXY
27	29	87.9	227	2	06SKX4_HCMV
28	29	87.9	227	2	06SKB5_HCMV
29	29	87.9	258	1	UPPS_THEAO
30	29	87.9	258	1	UPPS_THEAO
31	29	87.9	258	2	Q9M2T5_ARATH

32	29	87.9	258	2	Q6MEF4_PARUW	Q6MEF4_parchlamyd
33	29	87.9	262	2	Q863K2_PIG	Q863K2_sus scrofa
34	29	87.9	297	2	Q8AV24_FUGRU	Q8AV24_fugu rubrip
35	29	87.9	339	2	Q60ZM4_CAEBR	Q60ZM4_caenorhabdi
36	29	87.9	348	2	Q75D24_ASHGO	Q75D24_ashya goss
37	29	87.9	369	2	Q73VU4_MYCPA	Q73VU4_mycobacteri
38	29	87.9	370	1	DDL_MYCBO	Q7CX19_mycobacteri
39	29	87.9	373	1	DDL_MYCSM	Q9ZG10_mycobacteri
40	29	87.9	373	1	DDL_MYCTU	P95114_mycobacteri
41	29	87.9	373	1	Q18197_CAEBL	Q18197_caenorhabdi
42	29	87.9	384	1	DDL_MYCLB	Q9CB60_mycobacteri
43	29	87.9	491	1	ZAPR_PROMI	Q11137_proteus mir
44	29	87.9	491	1	Q85374_PROMI	Q85374_proteus mir
45	29	87.9	555	2	Q51AD3_BACRO	Q51AD3_bacteroides
46	29	87.9	555	2	Q64OR5_BACPR	Q64GR5_bacteroides
47	29	87.9	635	2	Q9VUK7_DROME	Q9VUK7_drosophila
48	29	87.9	700	2	Q720Z1_LISNF	Q720Z1_listeria mo
49	29	87.9	1251	2	Q4YV48_PLABE	Q4YV48_plasmodium
50	29	87.9	1319	2	Q61EX3_CAEBR	Q61EX3_caenorhabdi
51	29	87.9	1435	2	Q7S924_NEUCR	Q7S924_neurospora
52	29	87.9	1435	2	Q7RTC8_PLAYO	Q7RTC8_plasmodium
53	29	87.9	1976	2	Q7YH13_RHOBR	Q7YH13_rhodnius pr
54	29	87.9	1976	2	Q6Z103_ORYSA	Q6Z103_oryza sativ
55	29	87.9	1976	2	Q6ME93_PARUW	Q6ME93_parchlamyd
56	29	87.9	1976	2	Q4PED0_USTWA	Q4PED0_ustilago ma
57	29	87.9	188	2	Q4SWW5_TETWG	Q4SWW5_tetradon n
58	29	87.9	207	2	Q8UP61_9H1Y1	Q8UP61_human immun
59	29	87.9	224	2	Q631P1_BURPS	Q631P1_burkholderi
60	29	87.9	226	2	Q4UIR4_RICR	Q4UIR4_rickettsia
61	29	87.9	229	2	Q8VS70_BORHE	Q8VS70_borrelia he
62	29	87.9	230	1	UPPS_BORBU	Q51146_borrelia bu
63	29	87.9	230	1	Q662P2_BORCA	Q662P2_borrelia ga
64	29	87.9	230	2	Q6KHG6_MYCMO	Q6KHG6_mycoplasma
65	29	87.9	236	2	Q9T241_PHYTN	Q9T241_phytophthor
66	29	87.9	236	2	Q52VA3_PHYTN	Q52VA3_phytophthor
67	29	87.9	251	2	Q9HSA3_HUMAN	Q9HSA3_homo sapien
68	29	87.9	285	2	Q9HW71_THENA	Q9HW71_thermoga
69	29	87.9	285	2	Q92493_HUMAN	Q92493_homo sapien
70	29	87.9	308	2	Q81J10_PLAF7	Q81J10_plasmodium
71	29	87.9	309	2	Q97308_PLAF7	Q97308_plasmodium
72	29	87.9	309	2	Q6LEW0_PLAF7	Q6LEW0_plasmodium
73	29	87.9	312	2	Q6SFP9_9BACT	Q6SFP9_uncultured
74	29	87.9	337	2	Q60M40_CAEBR	Q60M40_caenorhabdi
75	29	87.9	338	2	Q9H5A4_HUMAN	Q9H5A4_homo sapien
76	29	87.9	354	2	Q91RS0_GVCP	Q91RS0_cydia pomon
77	29	87.9	358	2	Q7PA00_FUSNV	Q7PA00_fusobacteri
78	29	87.9	359	2	Q5TWS2_ANOCA	Q5TWS2_anopheles g
79	29	87.9	360	1	DDL_CORGL	Q8HPQ9_corynebacte
80	29	87.9	361	1	DDL_CORGL	Q8HPQ9_corynebacte
81	29	87.9	361	2	Q8N694_HUMAN	Q8N694_homo sapien
82	29	87.9	361	2	Q8N694_HUMAN	Q8N694_homo sapien
83	29	87.9	362	2	Q9S051_BORBU	Q9S051_borrelia bu
84	29	87.9	363	2	Q5YH77_NOCFA	Q5YH77_nocardia fa
85	29	87.9	365	2	Q6NHR6_CORNI	Q6NHR6_corynebacte
86	29	87.9	368	2	Q86G14_TOXSO	Q86G14_toxoplasma
87	29	87.9	370	2	Q5XYW3_BORCA	Q5XYW3_borrelia ga
88	29	87.9	370	2	Q9R2W7_BORBU	Q9R2W7_borrelia bu
89	29	87.9	370	2	Q9S003_BORBU	Q9S003_borrelia bu
90	29	87.9	370	2	Q9S096_BORBU	Q9S096_borrelia bu
91	29	87.9	370	2	Q9S0C8_BORBU	Q9S0C8_borrelia bu
92	29	87.9	370	2	Q9S0F9_BORBU	Q9S0F9_borrelia bu
93	29	87.9	373	2	Q5XZ68_BORCA	Q5XZ68_borrelia ga
94	29	87.9	373	2	Q5XZ68_BORCA	Q5XZ68_borrelia ga
95	29	87.9	375	2	Q8XJTB_CLOPE	Q8XJTB_photobacter
96	29	87.9	380	2	Q4XFR0_PLACH	Q4XFR0_plasmodium
97	29	87.9	384	2	Q6Z8B1_CAEBR	Q6Z8B1_caenorhabdi
98	29	87.9	390	2	Q8PG20_XANAC	Q8PG20_xanthomonas
99	29	87.9	407	2	Q9N3V7_CAEBL	Q9N3V7_caenorhabdi
100	29	87.9	412	2	Q87P22_VIBPA	Q87P22_vibrio para
101	29	87.9	423	2	Q5H3V1_XANOR	Q5H3V1_xanthomonas
102	29	87.9	441	2	Q8WTM2_CAEBL	Q8WTM2_caenorhabdi
103	29	87.9	443	2	Q8A9Y4_BACIN	Q8A9Y4_bacteroides
104	29	87.9	446	2	Q7T2X4_ONCMY	Q7T2X4_oncorhynchu

105	28	84.8	452	2	062YN6	BRARE	062YN6	brachydanio	178	27	81.8	271	2	08DYO	STRB6	08dY0	streptococc
106	28	84.8	458	2	05ORV7	ENTHI	05ORV7	entameeba h	179	27	81.8	271	2	07B55	STRB6	07B55	streptococc
107	28	84.8	464	1	OLEM	RANCA	007081	rana cateeb	180	27	81.8	273	2	05RNS	ASHRO	05RNS	ashro goss
108	28	84.8	468	2	067370	AOUNE	067370	aquifex aeo	181	27	81.8	277	2	05R77	ENTHO	05R77	entho
109	28	84.8	470	2	09H5H6	HUMAN	09H566	homo sapien	182	27	81.8	277	2	087X1	PYRBU	087X1	pyrococcus
110	28	84.8	493	2	086227	HUMAN	086227	homo sapien	183	27	81.8	277	2	087X0	STRAD	087X0	staphylococ
111	28	84.8	493	2	0SR9V4	PONYA	0SR9V4	pongo pygma	184	27	81.8	286	2	08CD13	STRAS	08CD13	staphylococ
112	28	84.8	497	1	NAS28	CAEEL	P86061	caenorhabdi	185	27	81.8	286	2	08NYU3	STRAW	08NYU3	staphylococ
113	28	84.8	514	2	062913	RAT	062913	rattus norv	186	27	81.8	291	2	050P2	ENTHI	050P2	entameeba h
114	28	84.8	520	2	05AC27	CANAL	05AC27	canidia alb	187	27	81.8	297	2	08M6X4	GNBOP	08M6X4	gnbop
115	28	84.8	557	2	07NBUS	MYCANL	07NBUS	mycoplasma	188	27	81.8	297	1	Y379	CAMJE	Y379	camje
116	28	84.8	576	2	06ARY5	DESPS	06ARY5	desulfoalba	189	27	81.8	297	2	04HFR4	CAMCO	04HFR4	camco
117	28	84.8	591	2	050SG0	ENTHI	050SG0	entamoeba h	190	27	81.8	297	2	04HMS9	CAMLA	04HMS9	camla
118	28	84.8	613	2	05ZJ91	CHICK	05ZJ91	gallus gall	191	27	81.8	297	2	05HW88	CAMJR	05HW88	camjr
119	28	84.8	676	2	09H5A7	HUMAN	09H57	homo sapien	192	27	81.8	304	1	WRK29	BARTH	WRK29	barth
120	28	84.8	715	2	05CRU3	CRYPV	05CRU3	cryptospori	193	27	81.8	304	1	Y1748	MOISU	Y1748	moisu
121	28	84.8	717	2	05CLG2	CRYPV	05CLG2	cryptospori	194	27	81.8	311	2	08FVNE	MOUSE	08FVNE	mouse
122	28	84.8	719	2	09H5A5	HUMAN	09H55	homo sapien	195	27	81.8	318	2	08GH19	ECOLI	08GH19	ecoli
123	28	84.8	742	1	CD44	HUMAN	P16070	h cd44 anti	196	27	81.8	321	2	07R0Z2	ANOGA	07R0Z2	anoga
124	28	84.8	742	2	09UJ36	HUMAN	09UJ6	homo sapien	197	27	81.8	321	2	05CHB0	CYPHO	05CHB0	cyphe
125	28	84.8	878	2	04UBM4	THEAN	04UBM4	thelateria d	198	27	81.8	322	2	07RW35	BRARE	07RW35	brare
126	28	84.8	1004	2	073K22	TREDE	073K22	treptonema d	199	27	81.8	322	2	05T257	BRARE	05T257	brare
127	28	84.8	1022	2	04RVG8	TETNG	04RV8	tetradon n	200	27	81.8	324	2	051188	MAGCR	051188	magcr
128	28	84.8	1024	1	CAR12	HUMAN	09MP4	homo sapien	201	27	81.8	326	2	09ZEX9	HELPI	09ZEX9	helpy
129	28	84.8	1061	2	05VXH9	DROME	05VXH9	tromophila	202	27	81.8	328	2	09ZN25	HELPI	09ZN25	helpy
130	28	84.8	1221	2	070139	LOTFA	070139	lotus japon	203	27	81.8	329	2	06HN67	BACHEL	06HN67	bachel
131	28	84.8	1446	2	04MTH8	THEPA	04MTH8	thelateria p	204	27	81.8	331	2	09XU14	CAREL	09XU14	carel
132	28	84.8	3064	2	04MTH8	THEPA	04MTH8	thelateria p	205	27	81.8	331	2	081HN8	BACCR	081HN8	baccr
133	28	84.8	3268	2	06C10	PLAT7	06C10	pseudomonas	206	27	81.8	332	2	07TS06	MOUSE	07TS06	mouse
134	27	81.8	38	2	05C0C1	SCHRA	05C0C1	schistosoma	207	27	81.8	334	2	061M03	CABER	061M03	caber
135	27	81.8	43	2	04W12	PLABE	04W12	plasmodium	208	27	81.8	334	2	04RFZ5	TETNG	04RFZ5	tetng
136	27	81.8	72	2	04Z0M1	PLABE	04Z0M1	plasmodium	209	27	81.8	335	2	07TS09	MOUSE	07TS09	mouse
137	27	81.8	103	2	04KRG5	PLABE	04KRG5	plasmodium	210	27	81.8	338	1	YYAD	BACSU	YYAD	bacsu
138	27	81.8	110	2	04FDM2	PIGE	04FDM2	pius scotia	211	27	81.8	347	2	05H614	XANOR	05H614	xanor
139	27	81.8	116	2	0899X1	CLOTE	0899X1	helicodrilum	212	27	81.8	354	2	093J97	9FIRM	093J97	9firm
140	27	81.8	122	2	07VGN1	HELEA	07VGN1	helicodrilum	213	27	81.8	354	2	09K1S1	CAMJE	09K1S1	camje
141	27	81.8	128	2	04XQ24	PLABE	04XQ24	plasmodium	214	27	81.8	357	2	081B05	BACCR	081B05	baccr
142	27	81.8	140	2	075Z21	SPBPA	075Z21	sphingomonas	215	27	81.8	357	2	081MX5	BACCN	081MX5	baccn
143	27	81.8	140	2	07XK9	3BNT0	07XK9	human coxsa	216	27	81.8	357	2	06H330	BACCN	06H330	baccn
144	27	81.8	144	2	075027	3BNT0	075027	human coxsa	217	27	81.8	357	2	08X810	BACCE	08X810	bacce
145	27	81.8	146	2	083VF6	3BNT0	083VF6	human coxsa	218	27	81.8	360	2	08HO10	IXOPE	08HO10	ixope
146	27	81.8	146	2	065UD1	ORVSA	065UD1	oryza sativ	219	27	81.8	363	2	06IM18	HUMAN	06IM18	human
147	27	81.8	150	2	04O579	LEIMA	04O579	leihamnia	220	27	81.8	383	2	097X75	SULSO	097X75	sulso
148	27	81.8	150	2	075UC2	3BNT0	075UC2	human coxsa	221	27	81.8	386	2	05WL02	BACSK	05WL02	bacsk
149	27	81.8	152	2	075098	3BNT0	075098	human coxsa	222	27	81.8	391	2	061ZV3	CABER	061ZV3	caber
150	27	81.8	154	2	075ZJ2	3BPNR	075ZJ2	sphingomonas	223	27	81.8	396	2	022250	CAREL	022250	carel
151	27	81.8	154	2	08K2M1	3BACT	08K2M1	uncultured	224	27	81.8	407	2	04UB18	THEAN	04UB18	thean
152	27	81.8	154	2	06MB94	PARUT	06MB94	parachlamyd	225	27	81.8	409	2	08D9C9	VITAV	08D9C9	vitav
153	27	81.8	155	2	06BJP0	BARTH	06BJP0	arabidopsis	226	27	81.8	409	2	07ML11	VIBVU	07ML11	vibv
154	27	81.8	155	2	06ASPO	BORCA	06ASPO	borrelia ga	227	27	81.8	412	2	05ISX6	ECOLI	05ISX6	ecoli
155	27	81.8	172	2	07VFT1	HELIP	07VFT1	helicobacte	228	27	81.8	416	2	08KN58	PESEAE	08KN58	peae
156	27	81.8	177	2	06YDA3	DROME	06YDA3	drosophilid	229	27	81.8	433	2	04RMT4	TETNG	04RMT4	tetng
157	27	81.8	183	2	08POV2	METAC	08POV2	metaphosarc	230	27	81.8	453	2	08SUM4	ENCCU	08SUM4	enccu
158	27	81.8	190	2	05OTK5	ENTHI	05OTK5	entamoeba h	231	27	81.8	455	2	06PE87	MOUSE	06PE87	mouse
159	27	81.8	190	2	05DGD1	SCHJA	05DGD1	schistosoma	232	27	81.8	457	2	04RLU6	TETNG	04RLU6	tetng
160	27	81.8	191	2	05R194	PLABE	05R194	idiomarina	233	27	81.8	458	2	05T3V6	HUMAN	05T3V6	human
161	27	81.8	203	2	04Y4V7	PLABE	04Y4V7	sphingomonas	234	27	81.8	458	2	018874	CAREL	018874	carel
162	27	81.8	204	2	075ZJ3	3BPNR	075ZJ3	chromobacte	235	27	81.8	466	2	0616D6	PLABE	0616D6	plabe
163	27	81.8	204	2	07NM99	CHRYO	07NM99	nocardiella fa	236	27	81.8	466	2	089XM5	BRADA	089XM5	brada
164	27	81.8	210	2	05YPG6	NOCRA	05YPG6	pasteurella	237	27	81.8	468	2	04MYR8	THEPA	04MYR8	theapa
165	27	81.8	215	2	09CM74	DASUM	09CM74	helicobacte	238	27	81.8	469	2	04X138	ASPEU	04X138	aspeu
166	27	81.8	223	2	07P8M6	RICST	07P8M6	helicobacte	239	27	81.8	475	2	06F198	MESPL	06F198	mespl
167	27	81.8	227	2	024881	HELPI	024881	rickettsia	240	27	81.8	477	2	NOE3	HUMAN	NOE3	human
168	27	81.8	248	1	Y754	RICCN	062H17	rickettsia	241	27	81.8	478	1	NOE3	RAT	NOE3	rat
169	27	81.8	248	1	Y754	RICCN	066455	mus musculu	242	27	81.8	478	1	NOE3	RAT	NOE3	rat
170	27	81.8	256	2	06PAB6	MOUSE	06PAB6	mus musculu	243	27	81.8	478	1	NOE3	RAT	NOE3	rat
171	27	81.8	257	2	060887	SGAMW	060887	uncultured	244	27	81.8	482	2	06IMD0	HUMAN	06IMD0	human
172	27	81.8	259	2	076128	GNBOP	076128	gnbop	245	27	81.8	484	2	06F838	ACTIAD	06F838	actiobact
173	27	81.8	266	2	076K11	GNBOP	076K11	parnasstus	246	27	81.8	484	2	0616M8	BOMMO	0616M8	bommyx mori
174	27	81.8	269	2	076129	GNBOP	076129	parnasstus	247	27	81.8	486	2	08VPW3	9FIRM	08VPW3	9firm
175	27	81.8	269	2	076123	GNBOP	076123	parnasstus	248	27	81.8	487	2	04HEC1	CAMCO	04HEC1	camco
176	27	81.8	269	2	076K02	GNBOP	076K02	parnasstus	249	27	81.8	488	2	04HLM0	CAMLA	04HLM0	camla
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SUMMARIES

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3	29	87.9	329	2	US-09-107-532A-3780 Sequence 3780, Ap
4	29	87.9	509	2	US-09-543-681A-5944 Sequence 5944, Ap
5	28	84.8	177	2	US-08-938-669A-30 Sequence 30, Appl
6	28	84.8	177	2	US-09-306-828-30 Sequence 30, Appl
7	28	84.8	295	2	US-09-949-016-9143 Sequence 9143, Ap
8	28	84.8	361	1	US-07-946-497-6 Sequence 6, Appl
9	28	84.8	361	1	US-08-483-322-6 Sequence 6, Appl
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20	27	81.8	285	2	US-09-107-433-4723 Sequence 37087, A
21	27	81.8	356	2	US-09-270-767-52304 Sequence 53304, A
22	27	81.8	356	2	US-09-270-767-52304 Sequence 4571, Ap
23	27	81.8	367	2	US-09-543-681A-4571 Sequence 349, App
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172	25	75.8	1515	1	US-09-423-126-3	Sequence 5, Appl1	245	24	72.7	341	2	US-09-270-767-36518	Sequence 36518, Ap
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SUMMARIES

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4	29	87.9	82	US-10-424-599-240774	Sequence 240774, A
5	29	87.9	83	US-10-437-963-165869	Sequence 165869, A
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11	29	87.9	364	US-10-186-886-44	Sequence 44, Appl1
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21	28	84.8	27	US-10-425-115-279832	Sequence 279832, A
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77	28	84.8	361	5	US-10-482-029-255	Sequence 255, App
78	28	84.8	361	5	US-10-852-335A-131	Sequence 131, App
79	28	84.8	361	5	US-10-805-769-2	Sequence 2, Appl1
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94	28	84.8	493	4	US-10-741-601-343	Sequence 343, App
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107	28	84.8	535	4	US-10-741-601-336	Sequence 336, App	180	27	81.8	159	5	US-10-472-928-8912	Sequence 928, App	
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112	28	84.8	676	5	US-10-473-127-1268	Sequence 1268, Ap	185	27	81.8	165	4	US-10-574-760A-526	Sequence 326, App	
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127	28	84.8	742	3	US-09-983-000A-16	Sequence 16, Appl	200	27	81.8	180	458	4	US-09-565-529-2	Sequence 2, Appl1
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166	27	81.8	77	4	US-10-425-115-194250	Sequence 194250, Sequence 54955, A	239	27	81.8	219	478	4	US-10-123-262-138	Sequence 138, App
167	27	81.8	88	4	US-10-425-115-154955	Sequence 54955, A Sequence 273510, App	240	27	81.8	220	478	4	US-10-123-262-138	Sequence 138, App
168	27	81.8	90	4	US-10-424-599-273510	Sequence 273510, Sequence 206401, App	241	27	81.8	221	478	4	US-10-123-262-138	Sequence 138, App
169	27	81.8	92	4	US-10-424-599-206401	Sequence 206401, Sequence 266274, App	242	27	81.8	222	478	4	US-10-123-262-138	Sequence 138, App
170	27	81.8	93	4	US-10-424-599-266274	Sequence 266274, Sequence 204131, App	243	27	81.8	223	478	4	US-10-123-262-138	Sequence 138, App
171	27	81.8	105	4	US-10-425-115-204131	Sequence 204131, Sequence 186562, App	244	27	81.8	224	478	4	US-10-123-262-138	Sequence 138, App
172	27	81.8	122	4	US-10-425-115-186562	Sequence 186562, Sequence 366313, App	245	27	81.8	225	478	4	US-10-123-262-138	Sequence 138, App
173	27	81.8	140	4	US-10-437-963-126434	Sequence 126434, Sequence 126434, App	246	27	81.8	226	478	4	US-10-131-818A-138	Sequence 138, App

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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	87.9	85	US-10-467-657-7040	Sequence 7040, Ap
2	87.9	85	US-10-467-657-7972	Sequence 7972, Ap
3	87.9	565	US-11-079-463-7488	Sequence 7488, Ap
4	84.8	361	US-10-995-561-612	Sequence 612, App
5	84.8	361	US-11-130-206-6	Sequence 6, App1
6	84.8	395	US-10-995-561-614	Sequence 614, App
7	84.8	425	US-10-995-561-616	Sequence 8908, App
8	84.8	455	US-11-079-463-8908	Sequence 611, App
9	84.8	493	US-10-995-561-611	Sequence 610, App
10	84.8	535	US-10-995-561-610	Sequence 617, App
11	84.8	691	US-10-995-561-617	Sequence 2, App1
12	84.8	699	US-11-130-206-4	Sequence 4, App1
13	84.8	700	US-11-130-206-2	Sequence 615, App
14	84.8	742	US-10-995-561-615	Sequence 618, App
15	84.8	742	US-10-995-561-618	Sequence 184, App
16	84.8	742	US-11-169-041-184	Sequence 176, App
17	84.8	742	US-11-072-175-176	Sequence 11, App1
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19	84.8	1024	US-11-145-631-2	Sequence 49, App1
20	84.8	1070	US-11-147-047-49	Sequence 5, App1
21	84.8	1204	US-11-145-631-5	Sequence 8177, App
22	81.8	226	US-11-087-099-8177	Sequence 7554, App
23	81.8	226	US-11-188-298-7554	Sequence 8077, App
24	81.8	232	US-11-087-099-8077	Sequence 18486, A
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26	81.8	447	US-11-079-463-6421	Sequence 6421, App
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29	81.8	478	US-11-174-150-27	Sequence 27, App1
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35	81.8	572	US-11-188-298-15206	Sequence 15206, A
36	81.8	572	US-11-188-298-17546	Sequence 17546, A
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38	81.8	817	US-11-012-762-2	Sequence 2, App1
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41	81.8	238	US-11-079-463-6309	Sequence 10209, A
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69	81.8	485	US-11-096-568A-6562	Sequence 16948, A
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102	24	72.7	375	7	US-11-051-267-18	Sequence 18, Appl	176	23	69.7	165	7	US-11-176-830-462	Sequence 457, App
103	24	72.7	375	7	US-11-051-267-4	Sequence 4, Appl	177	23	69.7	165	7	US-11-176-830-467	Sequence 502, App
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106	24	72.7	376	7	US-11-096-568A-11828	Sequence 11828, A	180	23	69.7	165	7	US-11-176-830-1	Sequence 1, Appl
107	24	72.7	376	7	US-11-096-568A-11827	Sequence 11827, A	181	23	69.7	165	7	US-11-176-830-2	Sequence 2, Appl
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111	24	72.7	478	7	US-11-188-298-11023	Sequence 11023, A	185	23	69.7	165	7	US-11-176-830-6	Sequence 6, Appl
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114	24	72.7	505	7	US-11-188-298-12928	Sequence 17898, A	188	23	69.7	165	7	US-11-176-830-9	Sequence 9, Appl
115	24	72.7	516	7	US-11-188-298-12929	Sequence 6224, Ap	189	23	69.7	165	7	US-11-176-830-10	Sequence 10, Appl
116	24	72.7	532	7	US-11-096-568A-10934	Sequence 2229, Ap	190	23	69.7	165	7	US-11-176-830-11	Sequence 11, Appl
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129	23	69.7	13	6	US-10-469-679A-48	Sequence 49, Appl	203	23	69.7	165	7	US-11-176-830-24	Sequence 24, Appl
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146	23	69.7	112	7	US-11-199-739-552	Sequence 34, Appl	220	23	69.7	165	7	US-11-176-830-41	Sequence 41, Appl
147	23	69.7	120	7	US-11-120-308-34	Sequence 34, Appl	221	23	69.7	165	7	US-11-176-830-42	Sequence 42, Appl
148	23	69.7	120	7	US-11-077-813A-16244	Sequence 16244, Ap	222	23	69.7	165	7	US-11-176-830-43	Sequence 43, Appl
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155	23	69.7	147	6	US-10-519-390-7	Sequence 9, Appl	229	23	69.7	165	7	US-11-176-830-50	Sequence 50, Appl
156	23	69.7	165	6	US-10-519-390-8	Sequence 8, Appl	230	23	69.7	165	7	US-11-176-830-51	Sequence 51, Appl
157	23	69.7	165	6	US-10-469-679A-5	Sequence 5, Appl	231	23	69.7	165	7	US-11-176-830-52	Sequence 52, Appl
158	23	69.7	165	6	US-10-469-679A-6	Sequence 6, Appl	232	23	69.7	165	7	US-11-176-830-53	Sequence 53, Appl
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160	23	69.7	165	6	US-10-469-679A-9	Sequence 9, Appl	234	23	69.7	165	7	US-11-176-830-55	Sequence 55, Appl
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166	23	69.7	165	7	US-11-176-830-102	Sequence 102, App	240	23	69.7	165	7	US-11-176-830-61	Sequence 61, Appl
167	23	69.7	165	7	US-11-176-830-280	Sequence 280, App	241	23	69.7	165	7	US-11-176-830-62	Sequence 62, Appl
168	23	69.7	165	7	US-11-176-830-280	Sequence 280, App	242	23	69.7	165	7	US-11-176-830-63	Sequence 63, Appl
169	23	69.7	165	7	US-11-176-830-280	Sequence 280, App	243	23	69.7	165	7	US-11-176-830-64	Sequence 64, Appl
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181	23	69.7	165	7	US-11-176-830-280	Sequence 280, App	255	23	69.7	165	7	US-11-176-830-76	Sequence 76, Appl
182	23	69.7	165	7	US-11-176-830-280	Sequence 280, App	256	23	69.7	165	7	US-11-176-830-77	Sequence 77, Appl
183	23	69.7	165	7	US-11-176-830-280	Sequence 280, App	257	23	69.7	165	7	US-11-176-830-78	Sequence 78, Appl
184	23	69.7	165	7	US-11-176-830-280	Sequence 280, App	258	23	69.7	165	7	US-11-176-830-79	Sequence 79,

98	29	67.4	209	6	ABU90061	Abu90061	Novel	hum	171	29	67.4	209	6	ABU83887	Abu83887	Human	sec
99	29	67.4	209	6	ABR68310	ABR68310	Human	sec	172	29	67.4	209	6	ABO08261	ABO08261	Human	PRO
100	29	67.4	209	6	ABU96363	ABU96363	Novel	hum	173	29	67.4	209	6	ABU02172	ABU02172	Novel	hum
101	29	67.4	209	6	ABU92794	ABU92794	Human	sec	174	29	67.4	209	6	ABR6126	ABR6126	Novel	hum
102	29	67.4	209	6	ABU69109	ABU69109	Human	PRO	175	29	67.4	209	6	ABR62425	ABR62425	Human	sec
103	29	67.4	209	6	ABO08871	ABO08871	Human	sec	176	29	67.4	209	6	ABR63285	ABR63285	Novel	hum
104	29	67.4	209	6	ABO02923	ABO02923	Human	sec	177	29	67.4	209	6	ABO00076	ABO00076	Novel	hum
105	29	67.4	209	6	ABR75077	ABR75077	Human	sec	178	29	67.4	209	6	ABR66676	ABR66676	Human	sec
106	29	67.4	209	6	ABR94839	ABR94839	Human	sec	179	29	67.4	209	6	ABR91094	ABR91094	Human	sec
107	29	67.4	209	6	ABU85812	ABU85812	Human	PRO	180	29	67.4	209	6	ABU94521	ABU94521	Human	PRO
108	29	67.4	209	6	ABU98187	ABU98187	Novel	hum	181	29	67.4	209	6	ABU79403	ABU79403	Human	PRO
109	29	67.4	209	6	ABU91893	ABU91893	Novel	hum	182	29	67.4	209	6	ABU87037	ABU87037	Novel	hum
110	29	67.4	209	6	ABU85986	ABU85986	Human	PRO	183	29	67.4	209	6	ABU94826	ABU94826	Human	PRO
111	29	67.4	209	6	ABU86427	ABU86427	Human	sec	184	29	67.4	209	6	ABU87037	ABU87037	Novel	hum
112	29	67.4	209	6	ABU67640	ABU67640	Human	sec	185	29	67.4	209	6	ABO04753	ABO04753	Human	PRO
113	29	67.4	209	6	ABU80668	ABU80668	Human	PRO	186	29	67.4	209	6	ABR670502	ABR670502	Human	sec
114	29	67.4	209	6	ABR95958	ABR95958	Human	sec	187	29	67.4	209	6	ABR66066	ABR66066	Human	PRO
115	29	67.4	209	6	ABR98976	ABR98976	Human	sec	188	29	67.4	209	6	ABR64783	ABR64783	Human	sec
116	29	67.4	209	6	ABR95976	ABR95976	Human	sec	189	29	67.4	209	6	ABR67708	ABR67708	Human	PRO
117	29	67.4	209	6	ABR92439	ABR92439	Human	sec	190	29	67.4	209	6	ABU93099	ABU93099	Human	PRO
118	29	67.4	209	6	ABO16425	ABO16425	Human	sec	191	29	67.4	209	6	ABU96058	ABU96058	Human	PRO
119	29	67.4	209	6	ABO15040	ABO15040	Human	sec	192	29	67.4	209	6	ABU91278	ABU91278	Human	PRO
120	29	67.4	209	6	ABR78461	ABR78461	Human	sec	193	29	67.4	209	6	ABU90371	ABU90371	Novel	hum
121	29	67.4	209	6	ABR85197	ABR85197	Human	sec	194	29	67.4	209	6	ABO09786	ABO09786	Human	sec
122	29	67.4	209	6	ABO00336	ABO00336	Novel	hum	195	29	67.4	209	6	ABO11058	ABO11058	Human	sec
123	29	67.4	209	6	ABO11668	ABO11668	Human	sec	196	29	67.4	209	6	ABR71112	ABR71112	Human	sec
124	29	67.4	209	6	ABO08315	ABO08315	Human	sec	197	29	67.4	209	6	ABU77720	ABU77720	Human	PRO
125	29	67.4	209	6	ABU89887	ABU89887	Human	sec	198	29	67.4	209	6	ABU91588	ABU91588	Human	PRO
126	29	67.4	209	6	ABU82382	ABU82382	Human	hum	199	29	67.4	209	6	ABU91588	ABU91588	Human	PRO
127	29	67.4	209	6	ABR65192	ABR65192	Human	hum	200	29	67.4	209	6	ABU84802	ABU84802	Human	PRO
128	29	67.4	209	6	ABR65192	ABR65192	Human	hum	201	29	67.4	209	6	ABU87720	ABU87720	Human	PRO
129	29	67.4	209	6	ABR65192	ABR65192	Human	sec	202	29	67.4	209	6	ABR69892	ABR69892	Human	sec
130	29	67.4	209	6	ABO03443	ABO03443	Human	sec	203	29	67.4	209	6	ABU80269	ABU80269	Human	PRO
131	29	67.4	209	6	ABO13363	ABO13363	Human	sec	204	29	67.4	209	6	ABU93538	ABU93538	Human	PRO
132	29	67.4	209	6	ABR65981	ABR65981	Human	sec	205	29	67.4	209	6	ABO10091	ABO10091	Human	sec
133	29	67.4	209	6	ABO13194	ABO13194	Human	sec	206	29	67.4	209	6	ABU10744	ABU10744	Human	sec
134	29	67.4	209	6	ABO13900	ABO13900	Human	sec	207	29	67.4	209	6	ABU95753	ABU95753	Human	PRO
135	29	67.4	209	6	ABU65803	ABU65803	Human	sec	208	29	67.4	209	6	ABU96962	ABU96962	Novel	hum
136	29	67.4	209	6	ABO07651	ABO07651	Human	PRO	209	29	67.4	209	6	ABR70807	ABR70807	Human	sec
137	29	67.4	209	6	ABR67286	ABR67286	Human	sec	210	29	67.4	209	6	ABU81550	ABU81550	Human	sec
138	29	67.4	209	6	ABO03838	ABO03838	Human	sec	211	29	67.4	209	6	ABO08566	ABO08566	Human	sec
139	29	67.4	209	6	ABO15889	ABO15889	Human	sec	212	29	67.4	209	6	ABO05158	ABO05158	Novel	hum
140	29	67.4	209	6	ABU56170	ABU56170	Human	sec	213	29	67.4	209	6	ABO08566	ABO08566	Human	sec
141	29	67.4	209	6	ABU65498	ABU65498	Human	PRO	214	29	67.4	209	6	ABR74162	ABR74162	Human	sec
142	29	67.4	209	6	ABU95443	ABU95443	Human	PRO	215	29	67.4	209	6	ABR39754	ABR39754	Human	sec
143	29	67.4	209	6	ABU71346	ABU71346	Human	PRO	216	29	67.4	209	6	ABR81051	ABR81051	Human	sec
144	29	67.4	209	6	ABO07956	ABO07956	Human	PRO	217	29	67.4	209	6	ABR81356	ABR81356	Human	sec
145	29	67.4	209	6	ABR69530	ABR69530	Human	sec	218	29	67.4	209	6	ABM01052	ABM01052	Human	sec
146	29	67.4	209	6	ABU69086	ABU69086	Human	sec	219	29	67.4	209	6	ABM77475	ABM77475	Human	sec
147	29	67.4	209	6	ABU69530	ABU69530	Human	sec	220	29	67.4	209	6	ABR86654	ABR86654	Human	sec
148	29	67.4	209	6	ABO01671	ABO01671	Human	PRO	221	29	67.4	209	6	ABM77475	ABM77475	Human	sec
149	29	67.4	209	6	ABU81473	ABU81473	Human	PRO	222	29	67.4	209	6	ABO28959	ABO28959	Human	sec
150	29	67.4	209	6	ABR60270	ABR60270	Human	sec	223	29	67.4	209	6	ABO31704	ABO31704	Human	sec
151	29	67.4	209	6	ABR68005	ABR68005	Human	sec	224	29	67.4	209	6	ADA76554	ADA76554	Novel	hum
152	29	67.4	209	6	ABR68005	ABR68005	Human	sec	225	29	67.4	209	6	ABM08121	ABM08121	Human	sec
153	29	67.4	209	6	ABR68005	ABR68005	Human	sec	226	29	67.4	209	6	ABO36026	ABO36026	Human	sec
154	29	67.4	209	6	ABR68615	ABR68615	Human	sec	227	29	67.4	209	6	ABO44165	ABO44165	Human	PRO
155	29	67.4	209	6	ABR72027	ABR72027	Human	sec	228	29	67.4	209	6	ADA78222	ADA78222	Human	sec
156	29	67.4	209	6	ABU85507	ABU85507	Human	PRO	229	29	67.4	209	6	ABO24960	ABO24960	Human	sec
157	29	67.4	209	6	ABU89197	ABU89197	Human	sec	230	29	67.4	209	6	ABO03228	ABO03228	Human	sec
158	29	67.4	209	6	ABU83277	ABU83277	Human	sec	231	29	67.4	209	6	ABR90484	ABR90484	Human	sec
159	29	67.4	209	6	ABU95133	ABU95133	Novel	hum	232	29	67.4	209	6	ABM17398	ABM17398	Human	sec
160	29	67.4	209	6	ABU90681	ABU90681	Novel	hum	233	29	67.4	209	6	ABR95144	ABR95144	Human	sec
161	29	67.4	209	6	ABU84192	ABU84192	Human	sec	234	29	67.4	209	6	ABR95449	ABR95449	Human	sec
162	29	67.4	209	6	ABU93843	ABU93843	Novel	hum	235	29	67.4	209	6	ABO21687	ABO21687	Human	sec
163	29	67.4	209	6	ABR65088	ABR65088	Human	sec	236	29	67.4	209	6	ABR97951	ABR97951	Human	sec
164	29	67.4	209	6	ABR68920	ABR68920	Human	sec	237	29	67.4	209	6	ABM77739	ABM77739	Human	sec
165	29	67.4	209	6	ABO06736	ABO06736	Human	sec	238	29	67.4	209	6	ABM77780	ABM77780	Human	sec
166	29	67.4	209	6	ABR99281	ABR99281	Human	sec	239	29	67.4	209	6	ABM28010	ABM28010	Human	sec
167	29	67.4	209	6	ABU57165	ABU57165	Human	PRO	240	29	67.4	209	6	ABM06291	ABM06291	Human	sec
168	29	67.4	209	6	ABU86117	ABU86117	Novel	hum	241	29	67.4	209	6	ABM03797	ABM03797	Human	sec
169	29	67.4	209	6	ABU82404	ABU82404	Novel	hum	242	29	67.4	209	6	ABM35248	ABM35248	Human	sec
170	29	67.4	209	6	ABU87415	ABU87415	Human	PRO	243	29	67.4	209	6	ABM26485	ABM26485	Human	sec

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:12 ; Search time 9.18367 Seconds
(without alignments)
104.769 Million cell updates/sec

Title: US-10-067-484-5
Perfect score: 43
Sequence: 1 FYATEVXDXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: PIR 80:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	79.1	398	2 G95205	glycosyl transferase
2	32	74.4	357	2 B81292	hypothetical prote
3	32	74.4	510	2 B60280	baclilolysin-like
4	32	74.4	829	2 E87305	TonB-dependent rec
5	32	74.4	1186	2 S70430	hypothetical prote
6	31	72.1	63	2 E69800	hypothetical prote
7	31	72.1	210	2 E75315	probable c-type cy
8	31	72.1	212	2 C43310	stringent starvati
9	31	72.1	418	2 E65014	xanthosine permeas
10	31	72.1	428	2 T06464	protein kinase (EC
11	31	72.1	433	2 A55333	monodehydroascorba
12	31	72.1	464	2 T03780	probable integral
13	31	72.1	710	2 T26742	hypothetical prote
14	31	72.1	1079	2 T18356	membrane protein p
15	31	72.1	1207	2 B88789	protein ZK1251.9
16	31	72.1	1211	2 T23210	hypothetical prote
17	30	69.8	114	2 S77061	transposase sl1066
18	30	69.8	176	2 AB0777	probable lipoprote
19	30	69.8	229	2 D90002	hypothetical prote
20	30	69.8	257	2 T34089	hypothetical prote
21	30	69.8	259	2 S76643	transposase slr051
22	30	69.8	261	2 S75081	transposase slr026
23	30	69.8	261	2 S77171	transposase sl1171
24	30	69.8	261	2 S77351	transposase sl1171
25	30	69.8	261	2 S76309	transposase slr035
26	30	69.8	305	2 C69465	diironoxenase redu
27	30	69.8	314	1 WMBB84	ribonucleoside-dip
28	30	69.8	314	2 H88391	protein K08D9.1 [f
29	30	69.8	433	2 T06407	monodehydroascorba

30	30	69.8	434	2 JU0182	monodehydroascorba
31	30	69.8	571	2 AG0144	D-lactate dehydrog
32	30	69.8	584	2 S06318	endoplasmic reticu
33	30	69.8	638	1 ISMSER	protein disulfide-
34	30	69.8	643	1 S32476	protein disulfide-
35	30	69.8	688	1 UC1469	beta-adrenergic-re
36	30	69.8	688	1 A39336	beta-adrenergic-re
37	30	69.8	882	2 E96931	hypothetical prote
38	30	69.8	1010	2 T36383	probable large ATP
39	29	67.4	115	2 H72643	hypothetical prote
40	29	67.4	230	2 B86824	two-component syst
41	29	67.4	256	2 A11204	molybdate ABC tran
42	29	67.4	326	2 T09259	cathepsin L-like p
43	29	67.4	326	2 E84812	hypothetical prote
44	29	67.4	347	2 S67159	probable membrane
45	29	67.4	388	2 D84992	hypothetical prote
46	29	67.4	390	2 C90288	hypothetical prote
47	29	67.4	392	2 G82746	hypothetical prote
48	29	67.4	395	2 C83788	galactokinase (imp
49	29	67.4	400	2 G89772	hypothetical prote
50	29	67.4	462	2 T26401	hypothetical prote
51	29	67.4	470	2 G85911	hypothetical prote
52	29	67.4	543	2 F91067	hypothetical prote
53	29	67.4	690	2 T01183	hypothetical prote
54	29	67.4	788	2 AF0122	probable membrane
55	29	67.4	929	2 S58824	rep-1 protein, for
56	29	67.4	929	2 A32495	hypothetical prote
57	29	67.4	1081	2 T00330	DNA mismatch repai
58	29	67.4	1126	2 JC4019	immunoglobulin Al
59	29	67.4	2004	2 F95133	hypothetical prote
60	28	65.1	139	2 T29394	hypothetical prote
61	28	65.1	161	2 T22196	hypothetical prote
62	28	65.1	161	2 T20676	hypothetical prote
63	28	65.1	201	2 G59096	hypothetical prote
64	28	65.1	214	2 S74663	peptide methionine
65	28	65.1	224	2 S24365	holocytochrome-c-s
66	28	65.1	230	2 F83697	ABC transporter (A
67	28	65.1	262	2 T17442	ylbT protein - Yer
68	28	65.1	262	2 E90156	undecaprenyl diph
69	28	65.1	267	2 AH0232	yersiniabactin bio
70	28	65.1	267	2 T30344	lrpA protein - Yer
71	28	65.1	267	2 T47050	hypothetical prote
72	28	65.1	273	2 T31506	positive transcrip
73	28	65.1	286	2 G84670	GDP-D-mannose dehy
74	28	65.1	309	2 C84167	exogastrolu-induci
75	28	65.1	325	2 A40084	hypothetical prote
76	28	65.1	327	2 C97663	conserved hypochet
77	28	65.1	327	2 AF2887	UDP-glucose 4-epim
78	28	65.1	339	2 B95187	UDPglucose 4-epime
79	28	65.1	339	2 C98054	mitogen-activated
80	28	65.1	369	2 S56638	mitogen-activated
81	28	65.1	371	2 T14915	mitogen-activated
82	28	65.1	375	2 T03971	probable sugar iso
83	28	65.1	386	2 T36425	sulfolipid biosynt
84	28	65.1	389	2 B90431	p54-gamma stress-ac
85	28	65.1	411	2 S43970	p54-beta stress-ac
86	28	65.1	426	2 T29169	hypothetical prote
87	28	65.1	431	2 T29716	2,2-dialkylglycine
88	28	65.1	431	2 A35173	aminotransferase,
89	28	65.1	435	2 AH3196	hypothetical prote
90	28	65.1	436	2 C89926	phosphoglycerate d
91	28	65.1	436	2 B95199	GMP-binding protei
92	28	65.1	436	2 H98065	hypothetical prote
93	28	65.1	436	2 C86719	hypothetical prote
94	28	65.1	437	2 T24953	monodehydroascorba
95	28	65.1	437	2 T48390	hypothetical prote
96	28	65.1	456	2 S76009	chromosome replica
97	28	65.1	458	2 A11269	protein kinase JNK
98	28	65.1	464	2 S71104	baclilolysin-like
99	28	65.1	510	2 A60280	zinc metalloprotei
100	28	65.1	510	2 AD1100	isomerase fuct (EC
101	28	65.1	604	2 F64081	probable serine/th
102	28	65.1	607	2 S62556	

monodehydroascorba
D-lactate dehydrog
endoplasmic reticu
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protein disulfide-
beta-adrenergic-re
beta-adrenergic-re
hypothetical prote
probable large ATP
hypothetical prote
two-component syst
molybdate ABC tran
cathepsin L-like p
hypothetical prote
probable membrane
hypothetical prote
hypothetical prote
galactokinase (imp
hypothetical prote
hypothetical prote
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hypothetical prote
probable membrane
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hypothetical prote
probable membrane
rep-1 protein, for
hypothetical prote
DNA mismatch repai
immunoglobulin Al
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
peptide methionine
holocytochrome-c-s
ABC transporter (A
ylbT protein - Yer
undecaprenyl diph
yersiniabactin bio
lrpA protein - Yer
hypothetical prote
hypothetical prote
positive transcrip
GDP-D-mannose dehy
exogastrolu-induci
hypothetical prote
conserved hypochet
UDP-glucose 4-epim
UDPglucose 4-epime
mitogen-activated
mitogen-activated
mitogen-activated
probable sugar iso
sulfolipid biosynt
p54-gamma stress-ac
p54-beta stress-ac
hypothetical prote
2,2-dialkylglycine
aminotransferase,
hypothetical prote
phosphoglycerate d
GMP-binding protei
hypothetical prote
monodehydroascorba
hypothetical prote
chromosome replica
protein kinase JNK
baclilolysin-like
zinc metalloprotei
isomerase fuct (EC
probable serine/th

103	28	65.1	621	2	JC7892	acyl-CoA dehydrog	176	27	62.8	446	2	F71069	hypothetical prote
104	28	65.1	634	2	H64508	hypothetical prote	177	27	62.8	449	2	A99286	conserved hypothec
105	28	65.1	652	2	T02001	hypothetical prote	178	27	62.8	459	2	B84936	UDP-N-acetylglucos
106	28	65.1	667	2	T01999	hypothetical prote	179	27	62.8	463	2	B72500	probab16c21-1-TRN
107	28	65.1	687	2	A41905	ferric vibriobacti	180	27	62.8	471	2	F71618	adenylsuccinate 1
108	28	65.1	715	2	D84480	Mutator-like trans	181	27	62.8	488	2	T48447	3-phenoethylsuccinylid
109	28	65.1	725	2	T20674	hypothetical prote	182	27	62.8	497	2	B83786	glyceral kinase gl
110	28	65.1	726	2	T40373	probable thiodoxo	183	27	62.8	499	2	H86815	hypothetical prote
111	28	65.1	760	2	S64023	AlrK protein - yea	184	27	62.8	506	2	T51702	amido-phosphoryl
112	28	65.1	897	2	T02808	conserved hypothec	185	27	62.8	516	2	UB0134	metan CUP1mi1-1-4-ba
113	28	65.1	962	2	G86479	FlAD7.6 protein -	186	27	62.8	527	2	T25126	serine CUP1mi1-1-4-ba
114	28	65.1	969	2	T03657	NAD ADP-ribosyltra	187	27	62.8	531	2	T11629	serine CUP1mi1-1-4-ba
115	28	65.1	1026	2	A49750	beta-galactosidase	188	27	62.8	555	2	B41492	58k antigenal - rich
116	28	65.1	1162	2	A12843	carbamoylphosphate	189	27	62.8	559	2	AB1153	hypothetical prote
117	28	65.1	1186	2	B97621	hypothetical prote	190	27	62.8	559	2	AC1512	hypothetical prote
118	28	65.1	1307	2	T35944	probable beta-gala	191	27	62.8	564	2	H70804	hypothetical prote
119	28	65.1	2077	1	MZBR24	240k tegument prot	192	27	62.8	576	2	T25375	hypothetical prote
120	28	65.1	2077	2	T44178	large tegument pro	193	27	62.8	614	2	T18539	hypothetical prote
121	28	65.1	2077	2	T43991	legum protein -	194	27	62.8	627	2	T19542	hypot (III) transpor
122	27	62.8	87	2	S39696	lywC protein - Bac	195	27	62.8	642	2	G64605	ferrous iron trans
123	27	62.8	88	2	D70010	hypothetical prote	196	27	62.8	642	2	D71904	protein kinase-lik
124	27	62.8	98	2	A98322	hypothetical prote	197	27	62.8	642	2	T45904	carriaine O-palmit
125	27	62.8	107	2	T46583	ferredoxin [import	198	27	62.8	658	2	A43462	hypothetical prote
126	27	62.8	125	2	B87297	conserved hypothec	199	27	62.8	658	2	G84663	probable protein k
127	27	62.8	127	2	B49300	protein-tyrosine k	200	27	62.8	676	2	S22258	hypothetical prote
128	27	62.8	143	2	B39061	hypothetical cytos	201	27	62.8	726	2	T26096	penicillin-binding
129	27	62.8	149	2	AF3343	hypothetical prote	202	27	62.8	730	2	A13480	USOC3.11 protein
130	27	62.8	154	2	AG1162	hypothetical prote	203	27	62.8	734	2	S44617	lanosterol synthas
131	27	62.8	160	2	A39061	conserved hypothec	204	27	62.8	749	2	T48782	Ompa family prote
132	27	62.8	161	2	AC0439	hypothetical prote	205	27	62.8	754	2	AC2807	hypothetical prote
133	27	62.8	165	2	D64648	hypothetical prote	206	27	62.8	760	2	B97586	hypothetical prote
134	27	62.8	167	2	B71939	hypothetical prote	207	27	62.8	764	2	T01441	protein F2401-1
135	27	62.8	172	2	B64978	hypothetical prote	208	27	62.8	770	2	H96649	radi-related DNA h
136	27	62.8	172	2	D85838	hypothetical prote	209	27	62.8	791	2	C97106	serine/threonine p
137	27	62.8	172	2	A90993	hypothetical prote	210	27	62.8	799	2	T48889	phenylalanyl-tRNA
138	27	62.8	179	2	D90167	conserved hypothec	211	27	62.8	801	2	S50660	phenylalanyl-tRNA
139	27	62.8	182	2	P83778	elongation factor	212	27	62.8	802	2	AF1227	DNA topoisomerase
140	27	62.8	185	2	D86711	elongation factor	213	27	62.8	804	2	CH4445	Villin - chicken
141	27	62.8	185	2	D95050	elongation factor	214	27	62.8	826	1	A31822	ORF MSY083 probabl
142	27	62.8	186	2	H97920	probable phosphat	215	27	62.8	834	2	T28250	probable peptidogl
143	27	62.8	190	2	T39622	probable regulator	216	27	62.8	882	2	AG1671	probable retroelem
144	27	62.8	208	2	AG0635	hypothetical prote	217	27	62.8	889	2	H84506	hypothetical prote
145	27	62.8	219	2	B64335	conserved hypothec	218	27	62.8	893	2	S63378	sensor protein kdp
146	27	62.8	247	2	C93579	probable phosphos	219	27	62.8	900	2	D97351	probable peptidogl
147	27	62.8	255	2	T24364	hypothetical prote	220	27	62.8	903	2	AG1299	protein-tyrosine k
148	27	62.8	260	2	C95380	conserved hypothec	221	27	62.8	932	2	A36931	protein-tyrosine k
149	27	62.8	268	2	F71712	prolipoprotein dia	222	27	62.8	993	2	A36873	Hadr type IC reacr
150	27	62.8	274	2	T18768	hypothetical prote	223	27	62.8	995	2	A11497	F13 protein - mou
151	27	62.8	285	1	J00851	site-specific DNA-	224	27	62.8	1000	2	S18827	hypothetical prote
152	27	62.8	285	2	AB0926	menadione biosyn	225	27	62.8	1048	2	H64459	126k pathogenicity
153	27	62.8	285	2	T31325	hypothetical 32.1k	226	27	62.8	1111	2	T09941	probable inner mem
154	27	62.8	292	2	J04099	annexin IX - fruit	227	27	62.8	1112	2	D82276	conserved revers
155	27	62.8	296	1	LJF093	signal-transducin	228	27	62.8	1120	2	B83498	telomerase repeat
156	27	62.8	323	2	B69252	protein T05A8.7 [i	229	27	62.8	1153	2	T51517	nitric-oxide synth
157	27	62.8	358	2	A88082	probable GTP-bind	230	27	62.8	1155	2	T33080	carbamoyl-phosphat
158	27	62.8	363	2	G75088	zinc finger protei	231	27	62.8	1162	2	AD3317	hypothetical prote
159	27	62.8	372	2	T38945	succinyl-diaminop	232	27	62.8	1186	2	T19334	chromodomain helic
160	27	62.8	384	2	F64048	voltage-gated pota	233	27	62.8	1418	2	T15232	hypothetical prote
161	27	62.8	393	2	T03947	adenosylmethionine	234	27	62.8	1518	2	T12880	hypothetical prote
162	27	62.8	400	2	S09636	pyruvate kinase - Bac	235	27	62.8	2052	2	T18290	FYVE finger-contai
163	27	62.8	401	2	T02378	glycolate oxidase	236	27	62.8	2180	2	A46182	polyprotein - echo
164	27	62.8	402	2	C93877	hypothetical prote	237	27	62.8	2352	2	C83229	probable non-ribos
165	27	62.8	408	2	AB5327	hypothetical prote	238	27	62.8	29	2	F83870	hypothetical prote
166	27	62.8	416	2	AB5340	folylpolyglutamate	239	27	62.8	74	2	F70526	hypothetical prote
167	27	62.8	423	2	S71036	protein kinase JNK	240	27	60.5	82	1	VCBPIK	coat protein B pre
168	27	62.8	427	2	S71037	protein kinase JNK	241	27	60.5	93	2	S75008	transposase ss1192
169	27	62.8	430	2	AH5638	pmbA protein [impo	242	27	60.5	101	2	S13701	ig kappa chain V r
170	27	62.8	431	2	HT1172	hypothetical prote	243	27	60.5	103	2	S13703	ig kappa chain V r
171	27	62.8					244	27	60.5				
172	27	62.8					245	27	60.5				
173	27	62.8					246	27	60.5				
174	27	62.8					247	27	60.5				
175	27	62.8					248	27	60.5				

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:05 ; Search time 54.4898 Seconds
(Without alignments)
129.479 Million cell updates/sec

Title: US-10-067-484-5
Perfect score: 43
Sequence: 1 FVATEVXDND 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Uniprot 05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	79.1	233	2	089R88 BRAVA
2	34	79.1	246	2	040106 SHIV1
3	34	79.1	346	1	FEN_PYRAB
4	34	79.1	398	2	097P77 STREP
5	34	79.1	449	2	088M47 LACPL
6	34	79.1	955	2	07P081 ANOGA
7	33	76.7	108	2	09J009 SHIV1
8	33	76.7	190	2	04XH19 PLACH
9	33	76.7	361	2	04Y0M3 PLACH
10	33	76.7	410	2	08ZXK3 PYRAB
11	33	76.7	436	2	08A9A2 BACTN
12	32	74.4	241	2	07XIP6 PLACT
13	32	74.4	319	2	073P18 TREDE
14	32	74.4	357	2	09PMK1 CAMTE
15	32	74.4	510	1	PRO2_LISMO
16	32	74.4	510	2	06E9N9 LISMO
17	32	74.4	510	2	06E9N9 LISMO
18	32	74.4	510	2	06EAC2 LISMO
19	32	74.4	510	2	06EAT1 LISMO
20	32	74.4	510	2	06EAG9 LISMO
21	32	74.4	510	2	06EAB8 LISMO
22	32	74.4	510	2	0724L0 LISMF
23	32	74.4	510	1	NRAM4 ARATH
24	32	74.4	570	2	04N3C1 THEPA
25	32	74.4	583	2	04UAL9 THEAN
26	32	74.4	594	2	05KUV5 GEOKA
27	32	74.4	624	2	0974Z9 DROME
28	32	74.4	788	2	04MMK4 BACCE
29	32	74.4	809	2	072LY1 LEPC
30	32	74.4	809	2	08EYF2 LEPC
31	32	74.4	829	2	09AAV8 CAUCR

105	30	69.8	69	2	OSUG9_9H1V1	OSUG9	human	immun	178	30	69.8	129	2	Q89CN6_BRAVA	Q89CN6	bradyrhizob
106	30	69.8	69	2	OSUCM4_9H1V1	OSUCM4	human	immun	179	30	69.8	139	2	Q75346_9H1V1	Q75346	human
107	30	69.8	69	2	OSUCM7_9H1V1	OSUCM7	human	immun	180	30	69.8	147	2	Q533V2_URSAR	Q533V2	ursus arcto
108	30	69.8	76	2	OSUROC6_9H1V1	OSUROC6	human	immun	181	30	69.8	147	2	Q533V4_AILME	Q533V4	ailuropoda
109	30	69.8	76	2	OS7MIT3_SALCH	OS7MIT3	salmonella	immun	182	30	69.8	147	2	Q533V5_PROLO	Q533V5	procyon lot
110	30	69.8	86	2	P89405_9H1V1	P89405	human	immun	183	30	69.8	147	2	Q533V6_POTFL	Q533V6	potos flavu
111	30	69.8	86	2	Q90AC4_9H1V1	Q90AC4	human	immun	184	30	69.8	147	2	Q533V7_PROVI	Q533V7	phoca vitul
112	30	69.8	87	2	Q9DXO7_9H1V1	Q9DXO7	human	immun	185	30	69.8	147	2	Q533V8_ERIBA	Q533V8	erignathus
113	30	69.8	86	2	Q10S29_9H1V1	Q10S29	human	immun	186	30	69.8	147	2	Q533V9_ZALCA	Q533V9	zalophus ca
114	30	69.8	82	2	Q75223_9H1V1	Q75223	human	immun	187	30	69.8	147	2	Q533Z0_CALUR	Q533Z0	callochinus
115	30	69.8	92	2	Q75328_9H1V1	Q75328	human	immun	188	30	69.8	147	2	Q533Z1_9CARN	Q533Z1	odobenus ro
116	30	69.8	93	2	Q97201_9H1V1	Q97201	human	immun	189	30	69.8	147	2	Q533Z2_9CARN	Q533Z2	mussetella fire
117	30	69.8	93	2	Q97195_9H1V1	Q97195	human	immun	190	30	69.8	147	2	Q533Z3_MUSFR	Q533Z3	meophilis me
118	30	69.8	93	2	Q97202_9H1V1	Q97202	human	immun	191	30	69.8	147	2	Q533Z4_MEPME	Q533Z4	lontxa cana
119	30	69.8	94	2	Q90035_9H1V1	Q90035	human	immun	192	30	69.8	147	2	Q533Z5_LONCN	Q533Z5	lontra cana
120	30	69.8	94	2	Q90037_9H1V1	Q90037	human	immun	193	30	69.8	147	2	Q533Z6_ENHLU	Q533Z6	emhydra lut
121	30	69.8	94	2	Q90038_9H1V1	Q90038	human	immun	194	30	69.8	147	2	Q533Z7_9CARN	Q533Z7	coepetus m
122	30	69.8	94	2	Q90039_9H1V1	Q90039	human	immun	195	30	69.8	147	2	Q533Z8_VIDLUV	Q533Z8	vulpes vulp
123	30	69.8	94	2	Q90040_9H1V1	Q90040	human	immun	196	30	69.8	147	2	Q533Z9_CANRF	Q533Z9	canis rufus
124	30	69.8	94	2	Q90041_9H1V1	Q90041	human	immun	197	30	69.8	147	2	Q534A0_CANFA	Q534A0	canis famil
125	30	69.8	94	2	Q90042_9H1V1	Q90042	human	immun	198	30	69.8	147	2	Q534A1_AILFU	Q534A1	ailurus ful
126	30	69.8	94	2	Q90043_9H1V1	Q90043	human	immun	199	30	69.8	150	2	Q5BGN6_9H1V1	Q5BGN6	human
127	30	69.8	94	2	Q90044_9H1V1	Q90044	human	immun	200	30	69.8	176	2	Q5PR45_SALPA	Q5PR45	salmonella
128	30	69.8	94	2	Q90045_9H1V1	Q90045	human	immun	201	30	69.8	176	2	Q825C2_SALTI	Q825C2	human
129	30	69.8	94	2	Q90046_9H1V1	Q90046	human	immun	202	30	69.8	194	2	Q681D9_9H1V1	Q681D9	human
130	30	69.8	94	2	Q90047_9H1V1	Q90047	human	immun	203	30	69.8	198	2	Q5VBL1_9H1V1	Q5VBL1	human
131	30	69.8	94	2	Q90048_9H1V1	Q90048	human	immun	204	30	69.8	201	2	Q8AEM3_9H1V1	Q8AEM3	human
132	30	69.8	94	2	Q90049_9H1V1	Q90049	human	immun	205	30	69.8	214	2	Q4P474_USRMA	Q4P474	uselligo ma
133	30	69.8	94	2	Q90050_9H1V1	Q90050	human	immun	206	30	69.8	220	2	Q7ZMF5_9H1V1	Q7ZMF5	human
134	30	69.8	94	2	Q90051_9H1V1	Q90051	human	immun	207	30	69.8	223	2	Q8AGD0_9H1V1	Q8AGD0	human
135	30	69.8	94	2	Q90052_9H1V1	Q90052	human	immun	208	30	69.8	228	2	Q40101_9H1V1	Q40101	human
136	30	69.8	94	2	Q90053_9H1V1	Q90053	human	immun	209	30	69.8	229	2	Q6G7L6_STRAS	Q6G7L6	staphylococ
137	30	69.8	94	2	Q90054_9H1V1	Q90054	human	immun	210	30	69.8	229	2	Q6GEV1_STRAC	Q6GEV1	staphylococ
138	30	69.8	94	2	Q90055_9H1V1	Q90055	human	immun	211	30	69.8	229	2	Q5HEA5_STRAC	Q5HEA5	staphylococ
139	30	69.8	94	2	Q90056_9H1V1	Q90056	human	immun	212	30	69.8	229	2	Q7ACB8_STRAC	Q7ACB8	staphylococ
140	30	69.8	94	2	Q90057_9H1V1	Q90057	human	immun	213	30	69.8	229	2	Q7AFC7_STRAM	Q7AFC7	staphylococ
141	30	69.8	95	2	Q74519_9H1V1	Q74519	human	immun	214	30	69.8	245	2	Q99SG3_STRAM	Q99SG3	staphylococ
142	30	69.8	95	2	Q74521_9H1V1	Q74521	human	immun	215	30	69.8	245	2	Q40094_9H1V1	Q40094	human
143	30	69.8	95	2	Q74522_9H1V1	Q74522	human	immun	216	30	69.8	246	2	Q40102_9H1V1	Q40102	human
144	30	69.8	95	2	Q74523_9H1V1	Q74523	human	immun	217	30	69.8	246	2	Q40103_9H1V1	Q40103	human
145	30	69.8	95	2	Q74524_9H1V1	Q74524	human	immun	218	30	69.8	246	2	Q40104_9H1V1	Q40104	human
146	30	69.8	95	2	Q74525_9H1V1	Q74525	human	immun	219	30	69.8	246	2	Q40105_9H1V1	Q40105	human
147	30	69.8	95	2	Q74526_9H1V1	Q74526	human	immun	220	30	69.8	246	2	Q40106_9H1V1	Q40106	human
148	30	69.8	95	2	Q74527_9H1V1	Q74527	human	immun	221	30	69.8	246	2	Q40107_9H1V1	Q40107	human
149	30	69.8	95	2	Q74528_9H1V1	Q74528	human	immun	222	30	69.8	246	2	Q40108_9H1V1	Q40108	human
150	30	69.8	95	2	Q74529_9H1V1	Q74529	human	immun	223	30	69.8	246	2	Q40109_9H1V1	Q40109	human
151	30	69.8	95	2	Q74530_9H1V1	Q74530	human	immun	224	30	69.8	246	2	Q40110_9H1V1	Q40110	human
152	30	69.8	95	2	Q74531_9H1V1	Q74531	human	immun	225	30	69.8	246	2	Q40111_9H1V1	Q40111	human
153	30	69.8	96	2	Q6THX0_9H1V1	Q6THX0	human	immun	226	30	69.8	259	2	Q40112_9H1V1	Q40112	human
154	30	69.8	102	2	Q77143_9H1V1	Q77143	human	immun	227	30	69.8	259	2	Q38831_STRAC	Q38831	staphylococ
155	30	69.8	105	2	Q6T105_9H1V1	Q6T105	human	immun	228	30	69.8	261	2	Q350V1_STRAC	Q350V1	staphylococ
156	30	69.8	106	2	Q37952_9H1V1	Q37952	human	immun	229	30	69.8	261	2	F73414_STRAC	F73414	staphylococ
157	30	69.8	106	2	Q37953_9H1V1	Q37953	human	immun	230	30	69.8	261	2	F73683_STRAC	F73683	staphylococ
158	30	69.8	106	2	Q37954_9H1V1	Q37954	human	immun	231	30	69.8	261	2	F73880_STRAC	F73880	staphylococ
159	30	69.8	112	2	Q8AT85_9H1V1	Q8AT85	human	immun	232	30	69.8	266	2	Q57495_STRAC	Q57495	staphylococ
160	30	69.8	112	2	Q8AT86_9H1V1	Q8AT86	human	immun	233	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
161	30	69.8	112	2	Q8AT87_9H1V1	Q8AT87	human	immun	234	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
162	30	69.8	112	2	Q8AT88_9H1V1	Q8AT88	human	immun	235	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
163	30	69.8	112	2	Q8AT89_9H1V1	Q8AT89	human	immun	236	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
164	30	69.8	112	2	Q8AT90_9H1V1	Q8AT90	human	immun	237	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
165	30	69.8	112	2	Q8AT91_9H1V1	Q8AT91	human	immun	238	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
166	30	69.8	112	2	Q8AT92_9H1V1	Q8AT92	human	immun	239	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
167	30	69.8	112	2	Q8AT93_9H1V1	Q8AT93	human	immun	240	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
168	30	69.8	112	2	Q8AT94_9H1V1	Q8AT94	human	immun	241	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
169	30	69.8	112	2	Q8AT95_9H1V1	Q8AT95	human	immun	242	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
170	30	69.8	114	2	Q8AT96_9H1V1	Q8AT96	human	immun	243	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
171	30	69.8	114	2	Q8AT97_9H1V1	Q8AT97	human	immun	244	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
172	30	69.8	114	2	Q8AT98_9H1V1	Q8AT98	human	immun	245	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
173	30	69.8	115	2	Q8AT99_9H1V1	Q8AT99	human	immun	246	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
174	30	69.8	115	2	Q8AT100_9H1V1	Q8AT100	human	immun	247	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
175	30	69.8	119	2	Q8AT101_9H1V1	Q8AT101	human	immun	248	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
176	30	69.8	129	2	Q8AT102_9H1V1	Q8AT102	human	immun	249	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap
177	30	69.8	129	2	Q8AT103_9H1V1	Q8AT103	human	immun	250	30	69.8	266	2	Q6R750_STRAC	Q6R750	cervus elap

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:21 ; Search time 19.3878 Seconds
(without alignments)
42.643 Million cell updates/sec

Title: US-10-067-484-5
Perfect score: 43
Sequence: 1 FVATEVXDXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep: *
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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	31	72.1	270	2	US-09-248-786A-14475 Sequence 14475, A
5	30	69.8	162	2	US-09-765-815-14 Sequence 14, Appl
6	30	69.8	433	1	US-08-417-492-2 Sequence 2, Appl
7	30	69.8	439	2	US-09-489-039A-8498 Sequence 8498, Appl
8	30	69.8	638	1	US-08-557-122A-38 Sequence 38, Appl
9	30	69.8	638	2	US-09-262-666-18 Sequence 38, Appl
10	30	69.8	698	2	US-09-949-016-10644 Sequence 10644, A
11	30	69.8	703	2	US-09-248-786A-14529 Sequence 14529, A
12	30	69.8	1027	2	US-09-107-532A-6675 Sequence 6675, Ap
13	30	69.8	1072	2	US-09-902-540-15572 Sequence 15572, A
14	30	69.8	1371	2	US-09-902-540-16024 Sequence 16024, A
15	30	69.8	2680	2	US-09-489-039A-7973 Sequence 7973, Ap
16	29	67.4	149	2	US-09-270-767-45126 Sequence 40126, A
17	29	67.4	149	2	US-09-270-767-45342 Sequence 55342, A
18	29	67.4	149	2	US-09-471-276-1517 Sequence 1517, Ap
19	29	67.4	347	2	US-09-538-092-753 Sequence 753, App
20	29	67.4	362	2	US-09-634-238-417 Sequence 417, App
21	29	67.4	644	2	US-09-949-016-82112 Sequence 8212, A
22	29	67.4	865	2	US-09-902-540-10416 Sequence 10416, A
23	29	67.4	877	2	US-09-165-386-5 Sequence 5, Appli
24	28	65.1	108	2	US-09-771-161A-179 Sequence 179, App
25	28	65.1	139	2	US-09-909-650B-27 Sequence 27, Appl
26	28	65.1	221	2	US-09-902-540-16354 Sequence 16354, A
27	28	65.1	270	2	US-09-489-039A-14315 Sequence 14315, A

28	28	65.1	308	2	US-09-328-352-6762 Sequence 6762, Ap
29	28	65.1	322	2	US-09-134-000C-6420 Sequence 6420, Ap
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31	28	65.1	346	2	US-09-107-433-4133 Sequence 4133, Ap
32	28	65.1	375	1	US-08-837-593-5 Sequence 5, Appli
33	28	65.1	375	2	US-09-623-034-2 Sequence 23, Appl
34	28	65.1	384	2	US-09-909-650B-23 Sequence 23, Appl
35	28	65.1	393	2	US-09-393-858-2 Sequence 2, Appli
36	28	65.1	393	2	US-09-393-858-2 Sequence 2, Appli
37	28	65.1	422	2	US-09-165-522-5 Sequence 38, Appl
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41	28	65.1	422	2	US-09-771-161A-269 Sequence 270, App
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52	28	65.1	434	6	5210025-7 Patent No. 5210025
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54	28	65.1	436	2	US-09-583-110-3142 Sequence 3142, Ap
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91	27	62.8	153	2	US-09-949-016-7661 Sequence 7661, Ap
92	27	62.8	153	2	US-09-711-164-368 Sequence 368, App
93	27	62.8	172	2	US-09-711-164-408 Sequence 408, App
94	27	62.8	186	2	US-09-583-110-3896 Sequence 3896, Ap
95	27	62.8	190	2	US-09-107-433-3585 Sequence 3585, Ap
96	27	62.8	196	2	US-09-248-786A-15195 Sequence 15195, A
97	27	62.8	198	2	US-09-525-223A-6 Sequence 6, Appli
98	27	62.8	245	2	US-09-105-058C-8 Sequence 8, Appli
99	27	62.8	266	2	US-09-602-787A-376 Sequence 376, App
100	27	62.8	266	2	US-09-602-787A-376 Sequence 376, App

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104	27	62.8	299	2	US-10-012-819-12	Sequence 12, Appl1	177	27	62.8	993	1	US-08-601-891-4	Sequence 4, Appl1
105	27	62.8	300	2	US-09-105-058C-4	Sequence 4, Appl1	178	27	62.8	993	1	US-09-021-324-4	Sequence 4, Appl1
106	27	62.8	300	2	US-09-105-028C-4	Sequence 6, Appl1	179	27	62.8	993	1	US-08-434-878-4	Sequence 4, Appl1
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108	27	62.8	355	2	US-09-331-568A-48	Sequence 28, Appl1	181	27	62.8	993	4	US-09-919-408A-4	Sequence 4, Appl1
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112	27	62.8	384	2	US-09-609-668-15	Sequence 15, Appl1	185	27	62.8	994	2	US-08-222-299-2	Sequence 2, Appl1
113	27	62.8	384	2	US-09-609-668-15	Sequence 15, Appl1	186	27	62.8	1000	1	US-08-434-878-2	Sequence 2, Appl1
114	27	62.8	384	2	US-09-411-628-16	Sequence 16, Appl1	187	27	62.8	1000	1	PCT-US95-03718-2	Sequence 2, Appl1
115	27	62.8	384	2	US-08-420-602B-16	Sequence 12, Appl1	188	27	62.8	1000	4	US-10-104-047-2509	Sequence 2509, Ap
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120	27	62.8	384	2	US-09-642-749-35	Sequence 35, Appl1	193	27	62.8	1248	2	US-09-949-016-10596	Sequence 10596, A
121	27	62.8	384	2	US-09-861-097-12	Sequence 12, Appl1	194	27	62.8	2052	2	US-09-045-201A-2	Sequence 2, Appl1
122	27	62.8	384	4	PCT-US94-08119-12	Sequence 12, Appl1	195	27	62.8	2052	2	US-09-615-062-2	Sequence 2, Appl1
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127	27	62.8	427	2	US-09-025-580-36	Sequence 36, Appl1	200	27	62.8	20	2	US-09-381-122A-5	Sequence 5, Appl1
128	27	62.8	427	2	US-09-642-749-34	Sequence 34, Appl1	201	27	62.8	20	2	US-09-381-122A-5	Sequence 5, Appl1
129	27	62.8	427	2	US-09-642-749-36	Sequence 36, Appl1	202	27	62.8	20	2	US-08-851-843A-154	Sequence 154, Ap
130	27	62.8	452	2	US-09-489-039A-12862	Sequence 12862, A	203	27	62.8	22	2	US-08-851-843A-160	Sequence 160, Ap
131	27	62.8	477	2	US-09-902-540-13329	Sequence 13329, A	204	27	62.8	22	2	US-08-574-549A-274	Sequence 274, Ap
132	27	62.8	480	2	US-09-248-796A-20820	Sequence 20820, A	205	27	62.8	22	2	US-08-574-549A-280	Sequence 280, Ap
133	27	62.8	481	2	US-07-912-122-4	Sequence 4, Appl1	206	27	62.8	22	2	US-08-854-050-154	Sequence 154, Ap
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143	27	62.8	633	2	US-09-417-197-45	Sequence 45, Appl1	216	27	62.8	22	2	US-10-054-295-154	Sequence 154, Ap
144	27	62.8	639	2	US-09-328-352-7786	Sequence 7786, Ap	217	27	62.8	22	2	US-10-054-295-160	Sequence 160, Ap
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146	27	62.8	757	2	US-09-177-650-89	Sequence 89, Appl1	219	27	62.8	22	2	US-09-438-486A-160	Sequence 160, Ap
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152	27	62.8	871	2	US-09-105-058C-20	Sequence 20, Appl1	225	27	62.8	22	2	US-09-721-456-256	Sequence 256, Ap
153	27	62.8	872	2	US-09-177-650-10609	Sequence 2, Appl1	226	27	62.8	22	2	US-09-721-456-256	Sequence 256, Ap
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:50:47 ; Search time 48.1633 Seconds
(without alignments)
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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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21	31	72.1	212	US-10-346-190-1	Sequence 1, Appl1
22	31	72.1	212	US-10-289-456-1	Sequence 1, Appl1
23	31	72.1	248	US-10-425-115-75493	Sequence 275493, A
24	31	72.1	381	US-10-282-122A-50829	Sequence 50829, A
25	31	72.1	401	US-10-437-963-173368	Sequence 173368, A
26	31	72.1	408	US-10-156-761-14852	Sequence 14852, A
27	31	72.1	428	US-10-732-923-10684	Sequence 10684, A

28	31	72.1	433	4	US-10-424-599-230372	Sequence 230372, A
29	31	72.1	433	4	US-10-424-599-243063	Sequence 243063, A
30	31	72.1	452	4	US-10-425-114-36611	Sequence 36611, A
31	31	72.1	453	4	US-10-425-115-193865	Sequence 193865, A
32	31	72.1	464	5	US-10-491-733-62	Sequence 62, Appl1
33	31	72.1	492	4	US-10-424-599-225164	Sequence 225164, A
34	31	72.1	500	5	US-10-866-527-38	Sequence 38, Appl1
35	31	72.1	516	4	US-10-282-122A-53219	Sequence 53219, A
36	31	72.1	524	4	US-10-437-963-146419	Sequence 146419, A
37	31	72.1	963	5	US-10-732-923-10686	Sequence 10686, A
38	30	69.8	44	4	US-10-431-596-70	Sequence 70, Appl1
39	30	69.8	52	4	US-10-424-599-182586	Sequence 182586, A
40	30	69.8	162	3	US-09-765-815-14	Sequence 14, Appl1
41	30	69.8	218	4	US-10-425-115-254298	Sequence 254298, A
42	30	69.8	229	3	US-09-815-242-12391	Sequence 12391, A
43	30	69.8	229	4	US-10-282-122A-44014	Sequence 44014, A
44	30	69.8	229	4	US-10-425-114-38922	Sequence 38922, A
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46	30	69.8	277	4	US-10-292-798-1708	Sequence 1708, App
47	30	69.8	327	4	US-10-156-761-9826	Sequence 9826, App
48	30	69.8	408	4	US-10-282-122A-53311	Sequence 53311, A
49	30	69.8	446	3	US-09-955-999-67	Sequence 67, Appl1
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55	30	69.8	537	4	US-10-425-114-67015	Sequence 67015, A
56	30	69.8	658	4	US-10-425-114-54318	Sequence 54318, A
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58	30	69.8	688	4	US-10-029-020-48	Sequence 48, Appl1
59	30	69.8	688	4	US-10-029-020-48	Sequence 48, Appl1
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61	30	69.8	688	5	US-10-788-197-25	Sequence 25, Appl1
62	30	69.8	703	4	US-10-425-115-253968	Sequence 253968, A
63	30	69.8	874	5	US-10-741-849-7216	Sequence 7216, App
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151	29	67.4	209	4	US-10-187-885-470	Sequence 470, App	224	29	67.4	209	4	US-10-184-654-470	Sequence 470, App
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153	29	67.4	209	4	US-10-187-887-470	Sequence 470, App	226	29	67.4	209	4	US-10-184-656-470	Sequence 470, App
154	29	67.4	209	4	US-10-187-888-470	Sequence 470, App	227	29	67.4	209	4	US-10-184-657-470	Sequence 470, App
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164	29	67.4	209	4	US-10-187-898-470	Sequence 470, App	237	29	67.4	209	4	US-10-184-667-470	Sequence 470, App
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173	29	67.4	209	4	US-10-184-630-470	Sequence 470, App	246	29	67.4	209	4	US-10-180-560-470	Sequence 470, App

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:04 ; Search time 8.77551 Seconds
(without alignments)
48.418 Million cell updates/sec

Title: US-10-067-484-5
Perfect score: 43
Sequence: 1 PYATEVXDD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	79.1	398	6	US-10-873-528-61
2	31	72.1	428	7	US-11-188-298-22499
3	31	72.1	963	7	US-11-188-298-15124
4	30	69.8	130	7	US-11-079-463-9460
5	30	69.8	688	7	US-11-113-424-48
6	30	69.8	688	7	US-11-113-424-49
7	30	69.8	688	7	US-11-040-218-25
8	30	69.8	688	7	US-11-040-218-27
9	29	67.4	146	7	US-11-055-822-812
10	29	67.4	186	7	US-11-055-822-810
11	29	67.4	209	6	US-10-194-487-470
12	29	67.4	209	6	US-10-195-883-470
13	29	67.4	209	6	US-10-195-888-470
14	29	67.4	209	6	US-10-195-889-470
15	29	67.4	209	6	US-10-226-486-29
16	29	67.4	326	7	US-11-096-568A-28259
17	29	67.4	376	7	US-11-079-463-5341
18	29	67.4	402	7	US-11-079-463-5274
19	29	67.4	454	7	US-11-079-463-5882
20	29	67.4	740	7	US-11-188-298-20749
21	29	67.4	877	7	US-11-087-099-7068
22	28	65.1	104	6	US-10-467-657-7314
23	28	65.1	214	6	US-11-079-463-8122
24	28	65.1	267	7	US-11-188-298-12836
25	28	65.1	287	7	US-11-079-463-8843

26	28	65.1	297	7	US-11-096-568A-4553	Sequence 4553, Ap
27	28	65.1	339	7	US-11-087-099-1188	Sequence 1188, Ap
28	28	65.1	339	7	US-11-087-099-9230	Sequence 9230, Ap
29	28	65.1	348	7	US-11-096-568A-4552	Sequence 4552, Ap
30	28	65.1	365	7	US-11-188-298-2445	Sequence 2445, Ap
31	28	65.1	369	7	US-11-188-298-6906	Sequence 6906, Ap
32	28	65.1	369	7	US-11-188-298-17616	Sequence 17616, A
33	28	65.1	376	7	US-11-188-298-5536	Sequence 5536, Ap
34	28	65.1	386	7	US-11-096-568A-4551	Sequence 4551, Ap
35	28	65.1	387	7	US-11-137-465-57	Sequence 57, Ap
36	28	65.1	422	6	US-10-857-780-21	Sequence 21, Ap
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38	28	65.1	422	7	US-11-180-044-5	Sequence 5, Ap
39	28	65.1	422	7	US-11-180-044-8	Sequence 8, Ap
40	28	65.1	422	7	US-11-180-044-12	Sequence 12, Ap
41	28	65.1	426	7	US-11-127-817-20	Sequence 20, Ap
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43	28	65.1	445	7	US-11-172-740-2494	Sequence 2494, Ap
44	28	65.1	464	7	US-11-127-817-19	Sequence 19, Ap
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46	28	65.1	607	7	US-11-188-298-834	Sequence 834, Ap
47	28	65.1	751	7	US-11-072-512-2507	Sequence 2507, Ap
48	28	65.1	752	7	US-11-072-512-2991	Sequence 2991, Ap
49	28	65.1	928	6	US-10-880-544-4	Sequence 4, Ap
50	28	65.1	3003	6	US-10-453-372-1080	Sequence 1080, Ap
51	28	65.1	3361	6	US-10-453-372-1082	Sequence 1082, Ap
52	27	62.8	261	6	US-10-821-234-1382	Sequence 1382, Ap
53	27	62.8	272	6	US-10-506-454-274	Sequence 274, Ap
54	27	62.8	314	7	US-11-129-143-98	Sequence 98, Ap
55	27	62.8	339	7	US-11-079-463-7909	Sequence 7909, Ap
56	27	62.8	337	7	US-11-087-099-2880	Sequence 2880, Ap
57	27	62.8	353	7	US-11-087-099-6054	Sequence 6054, Ap
58	27	62.8	363	7	US-11-087-099-7066	Sequence 7066, Ap
59	27	62.8	364	7	US-11-087-099-1264	Sequence 1264, Ap
60	27	62.8	417	7	US-11-096-568A-31333	Sequence 31333, A
61	27	62.8	422	7	US-11-172-740-1644	Sequence 1644, Ap
62	27	62.8	445	7	US-11-172-740-1643	Sequence 1643, Ap
63	27	62.8	452	7	US-11-172-740-2493	Sequence 2493, Ap
64	27	62.8	467	7	US-11-087-099-984	Sequence 984, Ap
65	27	62.8	488	7	US-11-096-568A-31332	Sequence 31332, A
66	27	62.8	488	7	US-11-096-568A-31331	Sequence 31331, A
67	27	62.8	515	7	US-11-093-274-38	Sequence 38, Ap
68	27	62.8	703	7	US-11-188-298-16926	Sequence 16926, A
69	27	62.8	703	7	US-11-096-568A-27899	Sequence 27899, A
70	27	62.8	717	7	US-11-096-568A-27898	Sequence 27898, A
71	27	62.8	749	7	US-11-087-099-6685	Sequence 6685, Ap
72	27	62.8	749	7	US-11-188-298-9767	Sequence 9767, Ap
73	27	62.8	759	7	US-11-188-298-17442	Sequence 17442, A
74	27	62.8	750	7	US-11-087-099-5543	Sequence 5543, Ap
75	27	62.8	750	7	US-11-188-298-16098	Sequence 16098, A
76	27	62.8	753	7	US-11-188-298-7467	Sequence 7467, Ap
77	27	62.8	778	7	US-11-096-568A-27897	Sequence 27897, A
78	27	62.8	788	7	US-11-079-463-5927	Sequence 5927, Ap
79	27	62.8	1066	7	US-11-072-512-2509	Sequence 2509, Ap
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82	26	60.5	34	7	US-11-207-078-256	Sequence 256, Ap
83	26	60.5	35	7	US-11-207-078-251	Sequence 251, Ap
84	26	60.5	42	7	US-11-207-078-96	Sequence 96, Ap
85	26	60.5	43	7	US-11-207-078-80	Sequence 80, Ap
86	26	60.5	47	7	US-11-207-078-42	Sequence 42, Ap
87	26	60.5	48	7	US-11-207-078-24	Sequence 24, Ap
88	26	60.5	78	7	US-11-096-568A-24032	Sequence 24032, A
89	26	60.5	116	7	US-11-096-568A-24031	Sequence 24031, A
90	26	60.5	120	7	US-11-096-568A-24030	Sequence 24030, A
91	26	60.5	132	7	US-11-038-676-22	Sequence 22, Ap
92	26	60.5	141	6	US-10-920-876-5	Sequence 5, Ap
93	26	60.5	141	6	US-10-920-876-6	Sequence 6, Ap
94	26	60.5	157	7	US-11-207-078-226	Sequence 226, Ap
95	26	60.5	155	6	US-10-793-626-2528	Sequence 2528, Ap
96	26	60.5	178	5	US-09-810-501-71	Sequence 71, Ap
97	26	60.5	178	7	US-11-167-831-24	Sequence 24, Ap
98	26	60.5	178	7	US-11-167-831-25	Sequence 25, Ap

99	26	60.5	178	7	US-11-167-831-26	Sequence 25, Appl	172	26	60.5	742	7	US-11-188-298-4229	Sequence 4217, Ap	
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101	26	60.5	178	7	US-11-167-831-28	Sequence 28, Appl	174	26	60.5	756	7	US-11-096-568A-30649	Sequence 14746, A	
102	26	60.5	178	7	US-11-167-831-29	Sequence 29, Appl	175	26	60.5	761	7	US-11-096-568A-14746	Sequence 11651, Ap	
103	26	60.5	178	7	US-11-167-831-30	Sequence 30, Appl	176	26	60.5	804	7	US-11-072-512-1161	Sequence 19556, A	
104	26	60.5	183	5	US-09-810-501-37	Sequence 37, Appl	177	26	60.5	811	7	US-11-188-298-19556	Sequence 462, Appl	
105	26	60.5	183	5	US-11-167-831-31	Sequence 31, Appl	178	26	60.5	826	6	US-10-878-556A-68	Sequence 222, Appl	
106	26	60.5	233	7	US-11-207-078-13	Sequence 14, Appl	179	26	60.5	884	7	US-11-077-407-078-122	Sequence 1474, Ap	
107	26	60.5	233	7	US-11-207-078-13	Sequence 14, Appl	180	26	60.5	911	7	US-11-096-568A-14745	Sequence 3179, Ap	
108	26	60.5	239	7	US-11-096-568A-31679	Sequence 31679, A	181	26	60.5	923	7	US-11-188-298-9370	Sequence 3708, Ap	
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111	26	60.5	287	7	US-11-188-298-4263	Sequence 4263, Ap	184	26	60.5	976	7	US-11-188-298-1112	Sequence 11203, Ap	
112	26	60.5	319	7	US-11-188-298-4263	Sequence 4263, Ap	185	26	60.5	988	7	US-11-207-078-112	Sequence 11202, Ap	
113	26	60.5	323	7	US-11-188-298-1590	Sequence 1590, Ap	186	26	60.5	1035	7	US-11-087-099-5013	Sequence 5013, Ap	
114	26	60.5	333	7	US-11-188-298-21977	Sequence 21977, A	187	26	60.5	1124	6	US-10-858-730-12	Sequence 12, Appl	
115	26	60.5	335	7	US-11-079-463-5389	Sequence 5389, Ap	188	26	60.5	1250	6	US-10-531-036-37	Sequence 37, Appl	
116	26	60.5	336	7	US-11-087-099-1620	Sequence 1620, Ap	189	26	60.5	1465	7	US-11-087-099-1192	Sequence 1792, Appl	
117	26	60.5	336	7	US-11-188-298-1610	Sequence 1610, Ap	190	26	60.5	1465	7	US-11-087-099-11059	Sequence 10059, Ap	
118	26	60.5	343	7	US-11-096-568A-8104	Sequence 8104, Ap	191	26	60.5	1465	7	US-11-188-298-11865	Sequence 1786, Ap	
119	26	60.5	349	7	US-11-096-568A-31677	Sequence 31677, A	192	26	60.5	1465	7	US-11-188-298-11865	Sequence 20298, A	
120	26	60.5	354	7	US-11-087-099-4127	Sequence 4127, A	193	26	60.5	1465	7	US-11-188-298-20298	Sequence 6, Appl	
121	26	60.5	380	7	US-11-096-568A-14911	Sequence 14911, A	194	26	60.5	1724	7	US-11-192-667-6	Sequence 6, Appl	
122	26	60.5	390	7	US-11-219-282-13	Sequence 13, Appl	195	26	60.5	1734	7	US-11-193-715-6	Sequence 94, Appl	
123	26	60.5	398	7	US-11-133-142-7	Sequence 7, Appl	196	26	60.5	2214	7	US-11-080-991-94	Sequence 94, Appl	
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125	26	60.5	404	7	US-11-096-568A-14910	Sequence 14910, A	198	26	60.5	4443	7	US-10-895-064-460	Sequence 460, Appl	
126	26	60.5	404	7	US-11-188-298-2276	Sequence 2276, Ap	199	26	60.5	4473	6	US-11-139-741-1610	Sequence 176, Appl	
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128	26	60.5	424	7	US-11-188-298-16105	Sequence 16105, A	201	26	60.5	42	7	US-11-031-026-116	Sequence 192, Appl	
129	26	60.5	425	7	US-11-087-099-1247	Sequence 1247, Ap	202	26	60.5	469	7	US-11-130-038-1192	Sequence 192, Appl	
130	26	60.5	432	7	US-11-188-298-1278	Sequence 1278, A	203	26	60.5	921	7	US-11-031-026-205	Sequence 205, Appl	
131	26	60.5	432	7	US-11-096-568A-14909	Sequence 14909, A	204	26	60.5	30	7	US-11-096-568A-54929	Sequence 5429, Ap	
132	26	60.5	436	7	US-11-172-740-2497	Sequence 2497, Ap	205	26	60.5	45	6	US-10-467-657-5920	Sequence 5920, Ap	
133	26	60.5	437	7	US-11-096-568A-8103	Sequence 8103, Ap	206	26	60.5	58.1	45	6	US-10-485-517-124	Sequence 124, Appl
134	26	60.5	438	7	US-11-087-099-2955	Sequence 2955, Ap	207	26	60.5	58.1	45	6	US-10-485-517-124	Sequence 294, Appl
135	26	60.5	439	7	US-11-172-740-2496	Sequence 2496, Ap	208	26	60.5	58.1	45	6	US-11-096-568A-15518	Sequence 15518, A
136	26	60.5	443	7	US-11-188-298-13028	Sequence 13028, A	209	26	60.5	58.1	45	7	US-11-096-568A-15518	Sequence 24651, A
137	26	60.5	443	7	US-11-188-298-16085	Sequence 16085, A	210	26	60.5	58.1	45	7	US-11-096-568A-24651	Sequence 92, Appl
138	26	60.5	444	7	US-11-188-298-13028	Sequence 13028, A	211	26	60.5	58.1	45	6	US-10-793-626-92	Sequence 2380, Appl
139	26	60.5	447	7	US-11-096-568A-8102	Sequence 8102, Ap	212	26	60.5	104	6	US-10-793-626-92	Sequence 15517, A	
140	26	60.5	460	7	US-11-172-740-2493	Sequence 2493, Ap	213	26	60.5	112	7	US-11-139-440-87	Sequence 87, Appl	
141	26	60.5	461	7	US-11-172-740-2498	Sequence 2498, Ap	214	26	60.5	123	7	US-11-096-568A-24649	Sequence 24649, A	
142	26	60.5	464	7	US-11-087-099-4129	Sequence 4129, Ap	215	26	60.5	144	7	US-11-096-568A-10348	Sequence 10348, A	
143	26	60.5	464	7	US-11-087-099-4129	Sequence 4129, Ap	216	26	60.5	152	7	US-11-096-568A-10348	Sequence 10145, A	
144	26	60.5	472	7	US-11-087-099-10553	Sequence 10553, A	217	26	60.5	158.1	174	7	US-11-079-463-15877	Sequence 5677, Ap
145	26	60.5	477	7	US-11-075-188-2-13300	Sequence 2, Appl	218	26	60.5	158.1	174	7	US-11-079-463-15877	Sequence 5677, Ap
146	26	60.5	477	7	US-11-188-298-14300	Sequence 14300, A	219	26	60.5	158.1	188	7	US-11-087-099-5013	Sequence 5013, Ap
147	26	60.5	480	7	US-11-132-142-6	Sequence 6, Appl	220	26	60.5	190	7	US-11-188-298-12302	Sequence 2392, Ap	
148	26	60.5	480	7	US-11-188-298-1665	Sequence 1665, Ap	221	26	60.5	194	7	US-11-096-568A-23350	Sequence 23350, Ap	
149	26	60.5	490	7	US-11-188-298-9166	Sequence 9166, Ap	222	26	60.5	196	7	US-11-096-568A-10134	Sequence 10134, Ap	
150	26	60.5	497	7	US-11-188-298-94614	Sequence 4614, Ap	223	26	60.5	197	7	US-11-096-568A-10134	Sequence 2391, Ap	
151	26	60.5	501	7	US-11-188-298-22165	Sequence 22165, A	224	26	60.5	214	7	US-11-096-568A-10133	Sequence 10133, Ap	
152	26	60.5	502	7	US-11-188-298-19312	Sequence 19312, A	225	26	60.5	219	7	US-11-096-568A-10133	Sequence 5815, Ap	
153	26	60.5	505	7	US-11-282-000-14	Sequence 14, Appl	226	26	60.5	240	7	US-10-511-538-827	Sequence 327, Appl	
154	26	60.5	515	7	US-11-132-142-8	Sequence 8, Appl	227	26	60.5	245	6	US-10-511-538-827	Sequence 399, Appl	
155	26	60.5	515	7	US-11-188-298-15437	Sequence 15437, A	228	26	60.5	247	7	US-11-000-463-999	Sequence 5866, Appl	
156	26	60.5	516	7	US-11-188-298-6618	Sequence 6418, Ap	229	26	60.5	247	7	US-11-096-568A-25549	Sequence 25549, Ap	
157	26	60.5	518	7	US-11-188-298-11340	Sequence 11340, A	230	26	60.5	249	7	US-11-096-568A-23350	Sequence 23350, Ap	
158	26	60.5	526	7	US-11-087-099-6670	Sequence 6670, Ap	231	26	60.5	258.1	249	7	US-11-096-568A-23350	Sequence 23350, Ap
159	26	60.5	536	7	US-11-188-298-13310	Sequence 13310, A	232	26	60.5	258.1	252	6	US-10-506-454-930	Sequence 930, Appl
160	26	60.5	550	7	US-11-052-554A-200	Sequence 13310, A	233	26	60.5	258.1	252	6	US-10-506-454-930	Sequence 930, Appl
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162	26	60.5	589	7	US-11-079-463-10153	Sequence 10153, A	235	26	60.5	275	7	US-11-096-568A-22436	Sequence 22436, Ap	
163	26	60.5	589	7	US-11-079-463-10153	Sequence 10153, A	236	26	60.5	293	7	US-11-096-568A-25549	Sequence 2617, Appl	
164	26	60.5	606	7	US-11-188-298-4068	Sequence 4068, Ap	237	26	60.5	293	7	US-11-096-568A-25549	Sequence 2617, Appl	
165	26	60.5	632	7	US-11-087-099-495	Sequence 495, Appl	238	26	60.5	304	7	US-11-096-568A-18870	Sequence 18870, Appl	
166	26	60.5	655	7	US-11-096-568A-30650	Sequence 30650, A	239	26	60.5	306	7	US-11-188-298-1480	Sequence 1480, Appl	
167	26	60.5	687	7	US-11-096-568A-14747	Sequence 14747, A	240	26	60.5	310	7	US-11-188-298-11559	Sequence 11566, A	
168	26	60.5	688	7	US-11-096-568A-6967	Sequence 6967, A	241	26	60.5	314	7	US-11-096-568A-18869	Sequence 18869, A	
169	26	60.5	692	7	US-11-079-463-7997	Sequence 7997, Ap	242	26	60.5	318	7	US-11-188-298-18377	Sequence 18377, Appl	
170	26	60.5	707	7	US-11-096-568A-6966	Sequence 6966, Ap	243	26	60.5	322	6	US-10-194-487-112	Sequence 172, Appl	
171	26	60.5	717	7	US-11-152-366-28	Sequence 28, Appl	244	26	60.5	58.1	322	6	US-10-195-883-172	Sequence 4219, Ap